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STIC-Biotech/ChemLib

From: Seharaseyon, Jegatheesan
Sent: Wednesday, September 06, 2006 10:29 AM
To: STIC-Biotech/ChemLib
Subject: Re: 10/659684

Hi,
Please search SEQ ID NO: 2 and 115 of 10/659684 in the commercial database.
Thanks.

Seyon.

J. Seharaseyon
Remsen 4C61,
Box 4C70.

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: 9-7-06
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:39:36 ; Search time 67.1143 Seconds
(without alignments)
1103.626 Million cell updates/sec

Title: US-10-659-684-2

Perfect score: 850
Sequence: 1 MRSSPGMEXIVICLWIFL.....LLOKMHQHSRTHGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*
9: geneeqp2005s:*
10: geneeqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	850	100.0	162	3 AAB18623	Aab18623 A human z
2	850	100.0	162	3 AAE13729	Aae13729 Human sol
3	850	100.0	162	5 AAU11965	Aau11965 Human int
4	850	100.0	162	6 ABR61407	Abri61407 Human IL-
5	850	100.0	162	7 AAE14932	Aae14932 Human int
6	850	100.0	162	7 ABU62893	Abu62893 Human int
7	850	100.0	162	7 ADE85808	Ade85808 Human int
8	850	100.0	162	7 ADF17046	Adf17046 Human alb
9	850	100.0	162	7 ADH44572	Adh44572 Human zal
10	850	100.0	162	7 ADI00908	Adi00908 Immunity-
11	850	100.0	162	8 ADH10501	Adh10501 Human int
12	850	100.0	162	8 ADJ25621	Adj25621 Human int
13	850	100.0	162	8 ADM41017	Adm41017 Human IL-
14	850	100.0	162	8 ADP12563	Adp12563 Protein e
15	850	100.0	162	8 ADP19731	Adp19731 Human zal
16	850	100.0	162	8 ADP70459	Adp70459 Human int
17	850	100.0	162	8 ADS19031	Ads19031 Full leng
18	850	100.0	162	9 ADV96355	Adv96355 Human zal
19	850	100.0	162	9 ADY20419	Ady20419 PRO polyp
20	850	100.0	162	9 ADY17792	Ady17792 PRO polyp
21	850	100.0	162	9 ADZ20501	Adz20501 Human int
22	850	100.0	162	9 AEB26428	Aeb26428 Human int
23	850	100.0	162	9 AED68671	Aed68671 Human int

24	850	100.0	162	10 AEB19679	Aeb19679 Human int
25	850	100.0	162	10 AEG05273	Aeg05273 Human IL-
26	840	98.8	160	9 AEA52828	Aea52828 Human int
27	837	98.5	162	8 ADY27249	Ady27249 Human int
28	831	97.8	162	7 AAE14934	Aae14934 Human int
29	758	89.2	147	7 AAE14933	Aae14933 Human int
30	708.5	83.4	742	7 ADF17042	Adf17042 Human alb
31	706	83.1	133	9 ADM43687	Adm43687 Mature hu
32	706	83.1	134	8 ADP70485	Adp70485 Codon opt
33	695.5	81.8	519	8 AAB18627	Aab18627 Ambro aci
34	695.5	81.8	519	5 AAU11971	Aau11971 MBP-human
35	695.5	81.8	519	7 ADH44655	Adh44655 Human zal
36	695.5	81.8	519	7 ADI00991	Adi00991 MBP (malt
37	695.5	81.8	519	8 ADP19814	Adp19814 Human zal
38	695.5	81.8	519	8 ADV96438	Adv96438 Human zal
39	695	81.8	131	8 ADS19023	Ads19023 Mature hu
40	695	81.8	131	9 ADM43684	Adm43684 Predicted
41	695	81.8	131	10 AEB19672	Aeb19672 Mature hu
42	661	77.8	133	9 ADM43680	Adm43680 Human int
43	656	77.2	133	9 ADM43682	Adm43682 Human int
44	650	76.5	131	9 ADM43678	Adm43678 Human int
45	648	76.2	152	10 AEB19682	Aeb19682 Bovine in

ALIGNMENTS

RESULT 1
AAB18623
ID AAB18623 standard; protein; 162 AA.
XX
AC AAB18623;
XX
DT 22-JAN-2001 (first entry)
XX
DE A human zalphall ligand polypeptide.
XX
KM zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.
XX
OS Homo sapiens.
XX
PN W0200053761-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WC-US006067.
XX
PR 09-MAR-1999; 99US-00264908.
PR 11-MAR-1999; 99US-00265992.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foeter DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR N-PSDB; AAA75552.
XX
PS WPI: 2000-565600/52.
XX
PT New human cytokine, designated zalphall ligand, useful for stimulating
PT the proliferation and/or development of hematopoietic cells in vitro and
PT in vivo, and for treating tumorigenesis.
XX
XX Disclosure; Page 205-206; 256pp; English.
CC The present sequence represents a human zalphall ligand polypeptide,
CC which is a cytokine. The zalphall ligand is useful for stimulating the
CC proliferation and development of haematopoietic cells in vitro and in
CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
CC for cloning the zalphall gene. The zalphall ligand is useful for treating
CC tumorigenesis. A zalphall ligand-aporin fusion toxin may be used for
CC treating leukaemia and lymphomas. Antagonists against zalphall ligand

PD 23-OCT-2001.
 XX
 PF 09-MAR-2000; 2000US-00522217.
 XX
 PR 09-MAR-1999; 99US-0123547P.
 PR 11-MAR-1999; 99US-0123904P.
 PR 01-JUL-1999; 99US-0142013P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 PI Grose JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX WPI; 2002-040208/05.
 DR N-PSDB; AAS20637.
 XX
 PT New zalphalil ligand polypeptides and polynucleotides, useful for
 PT stimulating proliferation, activation, differentiation and/or induction
 PT of inhibition of specialized cell function, or for stimulating an
 PT antigenic response.
 PS
 PS Claim 7; Col 125-126; 105pp; English.
 CC The present invention relates to the isolation of a novel cytokine,
 CC zalphalil ligand and the polynucleotide encoding it. The invention also
 CC gives the sequence for the zalphalil receptor and the polynucleotide
 CC encoding it. The zalphalil ligand polypeptide stimulates proliferation of
 CC natural killer (NK) cells or NK cell progenitors, the activation of NK
 CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
 CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
 CC reduces proliferation of B-cells stimulated with anti-19m antibodies. The
 CC zalphalil ligand polypeptide is also useful in preparing antibodies that
 CC bind to zalphalil ligand epitopes. The zalphalil ligand polynucleotides can
 CC be used as probes or primers to clone regions of a zalphalil ligand gene,
 CC and in gene therapy. Zalphalil ligand may also be used to identify
 CC inhibitors of its activity, to enhance the generation of anti-tumour
 CC responses with or without the infusion of donor lymphocytes, and to
 CC activate or stimulate the immune system. The present sequence represents
 CC human zalphalil ligand polypeptide. The cDNA encoding this is isolated
 CC from a cDNA library from activated human peripheral blood cells (hPBSCs)
 XX
 SQ Sequence 162 AA;
 Query Match 100.0%; Score 850; DB 5; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGNNRIVICLWYIFLGLTVHKSSSGQODRHIMRMQLIDIVDLKKNVNDLVEEF 60
 DB 1 MRSSPGNNRIVICLWYIFLGLTVHKSSSGQODRHIMRMQLIDIVDLKKNVNDLVEEF 60
 QY 61 LPAAEDVTNCEWSAFSCFOKALOKSANTGNNRINIVSIKKLKRKPPSTNAGRORQRL 120
 DB 61 LPAAEDVTNCEWSAFSCFOKALOKSANTGNNRINIVSIKKLKRKPPSTNAGRORQRL 120
 QY 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162
 DB 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162
 RESULT 4
 ABR61407 standard; protein; 162 AA.
 XX
 AC ABR61407;
 DT 12-AUG-2003 (first entry)
 XX
 DE Human IL-21 SEQ ID NO:19.
 XX
 KW arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
 KW immune cell activity; cancer; infectious disorder; antineumatic;
 KW antirheumatic; osteopathic; cytostatic; antibacterial;

KW vitruicide; antiparasitic; immunosuppressive; antidiabetic; dermatological;
 KW neuroprotective; antitumor; antiallergic; antianemic; hepatotropic;
 KW antitumor; antineoplastic; antineoplastic; antineoplastic; antineoplastic;
 KW antitumor; antineoplastic; antineoplastic; antineoplastic; antineoplastic;
 XX Homo sapiens.
 XX WO2003028630-A2.
 XX
 XX 10-APR-2003.
 XX
 XX 04-OCT-2002; 2002WO-US029839.
 XX
 XX 04-OCT-2001; 2001US-00972218.
 XX 17-APR-2002; 2002US-0373746P.
 XX
 XX (AMHP) WYETH.
 XX
 XX Carter L, Whiters MJ, Collins M, Young DA, Larsen G;
 PI Donaldson DP, Lowe LD, Dunnevi K, Ma M, Witek JS, Kasalan MT;
 PI Ungar M;
 XX WPI; 2003-430146/40.
 DR N-PSDB; ACC80873.
 DR
 XX
 XX Treating or preventing arthritic disorder, cancer or infectious disorders
 PT in a subject, involves administering a modulator of interleukin-21 or its
 PT receptor which modulate immune cell activity.
 PT
 PS Disclosure; Page 37; 176pp; English.
 XX
 XX The invention relates to a novel method for treating or preventing an
 XX arthritic disorder in a subject. The method involves administering to the
 XX subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
 XX optionally in combination with another therapeutic agent, to inhibit or
 XX reduce immune cell activity in the subject. The method is also useful for
 XX treating or preventing cancer or an infectious disorder, in a subject, by
 XX administering IL-21/IL-21R agonist, to increase immune cell activity. The
 XX method of the invention has antineoplastic, antitumor, antiparasitic,
 XX antiparasitic, cytostatic, antibacterial, vitruicide, antiparasitic,
 XX immunosuppressive, antidiabetic, neuroprotective, dermatological,
 XX antitumor, antineoplastic, antiallergic, antineoplastic, hepatotropic,
 XX antitumor, and antineoplastic activity. The method is useful for
 XX treating or preventing an arthritic disorder such as rheumatoid
 XX arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
 XX arthritis or ankylosing spondylitis, and also cancer such as solid
 XX tumour, soft tissue tumour or metastatic lesion, or an infectious
 XX disorder such as bacterial, viral or parasitic infection in a mammal,
 XX preferably human. A method of the invention is also useful for
 XX increasing the ability of a vaccine composition containing an antigen to
 XX elicit a protective immune response in a subject against the antigens.
 XX The antigen is from a pathogen such as virus, bacterium or protozoan, or
 XX from cancer or tumour cell antigen, or expressed on the surface of cancer
 XX cell. An alternative method of the invention is useful for modulating the
 XX activity of immune or haematopoietic cells and thus to treat or prevent a
 XX variety of immune disorders, such as autoimmune diseases, for example
 XX diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus
 XX erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,
 XX hepatitis, Graves' disease, graft versus host disease, and scleroderma.
 XX The present sequence is used in an exemplification of the invention
 XX
 SQ Sequence 162 AA;
 Query Match 100.0%; Score 850; DB 6; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGNNRIVICLWYIFLGLTVHKSSSGQODRHIMRMQLIDIVDLKKNVNDLVEEF 60
 DB 1 MRSSPGNNRIVICLWYIFLGLTVHKSSSGQODRHIMRMQLIDIVDLKKNVNDLVEEF 60
 QY 61 LPAAEDVTNCEWSAFSCFOKALOKSANTGNNRINIVSIKKLKRKPPSTNAGRORQRL 120
 DB 61 LPAAEDVTNCEWSAFSCFOKALOKSANTGNNRINIVSIKKLKRKPPSTNAGRORQRL 120

```
Db      61 LPAPEDVETNCESAFSCFQKAQLKSANTGNNERIINVSIKLKRKPSTNAGRQKRL 120
Qy      121 TCPSCDSEYKKPPKEFLERFKSLQKMIHQHLSRTHGSEDS 162
        |||||
Db      121 TCPSCDSEYKKPPKEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 5
AAE14932
ID      AAE14932 standard; protein; 162 AA.
XX
AC      AAE14932;
XX
DT      27-AUG-2003 (first entry)
XX
DE      Human interleukin-21 (IL-21).
XX
KW      Interleukin-21; IL-21; antagonist; cancer; inflammatory;
KW      autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW      systemic lupus erythematosus; myasthenia gravis; diabetes; human;
KW      zalphall ligand.
XX
OS      Homo sapiens.
XX
FH      Key                      Location/Qualifiers
FT      Region                  41..56
FT      Binding-site            44
FT      Binding-site            47
FT      Binding-site            /note= "Important for IL-21 binding to its receptor"
FT      Region                  57..68
FT      Region                  /label= A/B_loop
FT      Region                  69..84
FT      Region                  /label= Helix_B
FT      Region                  85..91
FT      Region                  /label= B/C_loop
FT      Region                  92..105
FT      Region                  /label= Helix_C
FT      Region                  106..134
FT      Region                  /label= C/D_loop
FT      Region                  135..148
FT      Region                  /label= Helix_D
FT      Binding-site            135
FT      Binding-site            /note= "Important for IL-21 binding to its receptor"
XX
XX      MO2003040313-A2.
XX
XX      15-MAY-2003.
XX
XX      28-OCT-2002; 2002MO-US034502.
XX
XX      05-NOV-2001; 2001US-0337586P.
XX
XX      (ZYMO ) ZYMOGENETICS INC.
XX
XX      Presnell SR, West JW, Novak JE;
XX      WPI; 2003-441547/41.
XX      DR      N-PSDB; AAD47852.
XX
XX      New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
XX      PT      and treating disorders with aberrant expression or activity of the IL-21
XX      PT      polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
XX      PT      diabetes.
XX
XX      Disclosure; Page 53-54; 71pp; English.
XX
XX      The invention relates to polynucleotides and polypeptides of interleukin-
XX      CC      21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
XX      CC      that is not detectable in receptor binding studies. The antagonists of
XX      CC      the invention have mutations in the D helix of the IL-21 molecule, and
XX      CC      can be used to inhibit the activity of IL-21 with its cognate receptor.
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```
CC      The IL-21 antagonists are useful for diagnosing and treating disorders
CC      CC      involving the aberrant expression or activity of the IL-21 polypeptide,
CC      CC      such as cancer, inflammatory and autoimmune disorders, including
CC      CC      rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
CC      CC      myasthenia gravis and diabetes. The polypeptides can also be used to
CC      CC      prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
CC      CC      and for enhancing in vivo killing of target tissues. The present sequence
CC      CC      is human IL-21 (originally designated zalphall ligand)
XX
XX      SO      Sequence 162 AA:
XX
XX      Query Match                      100.0%; Score 850; DB 7; Length 162;
XX      Best Local Similarity 100.0%; Pred. No. 2e-86;
XX      Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      1 MRSSPGNMERIVICLWVIFIGTLVHKSSSGODRHMIRMQLDIDYDLKNYVNDLVPEF 60
        |||||
Db      1 MRSSPGNMERIVICLWVIFIGTLVHKSSSGODRHMIRMQLDIDYDLKNYVNDLVPEF 60
Qy      61 LPAPEDVETNCESAFSCFQKAQLKSANTGNNERIINVSIKLKRKPSTNAGRQKRL 120
        |||||
Db      61 LPAPEDVETNCESAFSCFQKAQLKSANTGNNERIINVSIKLKRKPSTNAGRQKRL 120
Qy      121 TCPSCDSEYKKPPKEFLERFKSLQKMIHQHLSRTHGSEDS 162
        |||||
Db      121 TCPSCDSEYKKPPKEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 6
ABU62893
ID      ABU62893 standard; protein; 162 AA.
XX
XX      ABU62893;
XX
XX      15-SEP-2003 (first entry)
XX
XX      Human interleukin 21 (IL-21).
XX
XX      Human, MW-1; haematopoietin receptor superfamily chain; immunomodulator;
XX      KW      cytostatic; antibacterial; virucide; antineoplastic; gene therapy;
XX      KW      hematopoiesis; anaemia; immune response; cancer; infection;
XX      KW      transplanted organ; cytokine; receptor; interleukin 21; IL21.
XX
XX      OS      Homo sapiens.
XX
XX      US2003049798-A1.
XX
XX      13-MAR-2003.
XX
XX      04-OCT-2001; 2001US-00972218.
XX
XX      17-MAR-1998; 98US-00040005.
XX      PR      28-APR-2000; 2000US-00560766.
XX      PR      11-MAY-2000; 2000US-00569384.
XX
XX      (CART/) CARTER L.
XX      PA      (WHIT/) WHITTERS M J.
XX      PA      (COLL/) COLLINS M.
XX      PA      (YOUN/) YOUNG D A.
XX      PA      (DONA/) DONALDSON D D.
XX      PA      (LOWE/) LOWE L D.
XX      PA      (UNGE/) UNGER M.
XX
XX      Carter L, Whitters M, Collins M, Young DA, Donaldson DD,
XX      PI      Lowe LD, Unger M;
XX
XX      WPI; 2003-512354/48.
XX      DR      N-PSDB; ACD26729.
XX
XX      New fusion polypeptide for regulating hematopoiesis and immune responses,
XX      PT      comprises a fragment of a MW-1 polypeptide and a non-MW-1 fusion
XX      PT      polypeptide.
```

PS Disclosure; Page 10; 26pp; English.

XX The invention describes a fusion polypeptide comprising at least a
CC fragment of a WO-1 polypeptide and a non-WO-1 fusion polypeptide. The
CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of
CC anaemias) and/or immune responses (e.g. immune response to cancer,
CC infections or to a transplanted organ) and in identifying other members
CC of the haematopoietic superfamily, including cytokines and receptors. The
CC polynucleotide may be used to express recombinant protein for analysis,
CC characterisation or therapeutic use; and as markers for tissues or
CC chromosomes. The polypeptide and polynucleotide may also be used as
CC nutritional sources or supplements. This is the amino acid sequence of
CC human interleukin 21 (IL21), a cytokine receptor that can be used to
CC characterise the novel haematopoietic receptor of the invention

XX Sequence 162 AA;

Query Match 100.0%; Score 850; DB 7; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQDRHMRMQLDIVDQKNYVNDLVEPF 60
Db 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQDRHMRMQLDIVDQKNYVNDLVEPF 60

Qy 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRORHRL 120
Db 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRORHRL 120

Qy 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 7

ADBS808
ID ADBS808 standard; protein; 162 AA.

XX ADBS808;

DT 29-JAN-2004 (first entry)

XX Human interleukin-21.

XX Human; interleukin-21; immunosuppressive; antitumour; antiarthritic;
KW antiinflammatory; dermatological; ophthalmological; uropathic;
KW muscular-gen.; vasotropic; antidiabetic; antihypertensive; thymic;
KW neuroprotective; gastrointestinal-gen.; antipeptidic; gene therapy.

XX Homo sapiens.

XX WO2003087320-A2.

XX 23-OCT-2003.

XX 08-APR-2003; 2003WO-US010736.

XX 09-APR-2002; 2002US-0371038P.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Mo11 T, Strom TB, Zheng XX;

XX WPI; 2003-845317/78.

XX New substantially pure interleukin-21 polypeptide, useful for diagnosing,
PT treating and prognosticating autoimmune disorders, e.g. rheumatic
PT disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis
PT and myasthenia gravis.

XX Disclosure; SEQ ID NO 1; 65pp; English.

XX The present sequence is the protein sequence of human interleukin-21 (IL-

CC 21). The invention provides antagonists of the IL-21 receptor. These
CC include mutants of murine IL-21 in which the Gln residue at position 119
CC of the mature polypeptide is substituted by Asp or in which the Gln
CC residues at positions 114 and 119 of the mature polypeptide are both
CC replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell
CC activation. They preferably comprise a sequence that increases
CC circulating half-life, such as the FC region of an IgG molecule and may
CC further comprise an antigenic tag. Such antagonists inhibit cellular
CC proliferation in response to either anti-CD3 monoclonal antibodies or
CC anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with
CC IL-21. A claimed method of suppressing the immune response in a patient
CC comprises administering the IL-21 antagonist or a nucleic acid encoding
CC it. The method is used to treat an autoimmune disease such as rheumatic
CC disease, including connective tissue disease, dermatomyositis,
CC scleroderma, mixed connective tissue disease, or Bence's disease, or rheumatoid
CC polyarthritis, Reiter's syndrome, or Bence's disease, or rheumatoid
CC arthritis, type I diabetes, autoimmune disease of the thyroid such as
CC Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the
CC central nervous system such as multiple sclerosis, myasthenia gravis, or
CC encephalomyelitis, or an autoimmune disease selected from pemphigus
CC vulgaris, pemphigus vegetans, pemphigus foliaceus, Senear-Usher syndrome,
CC Brazilian pemphigus, psoriasis or inflammatory bowel disease (all
CC claimed).

XX Sequence 162 AA;

Query Match 100.0%; Score 850; DB 7; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQDRHMRMQLDIVDQKNYVNDLVEPF 60
Db 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQDRHMRMQLDIVDQKNYVNDLVEPF 60

Qy 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRORHRL 120
Db 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNNERIINVSIKLKRKPPSTNAGRORHRL 120

Qy 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 8

ADFL7046
ID ADFL7046 standard; protein; 162 AA.

XX ADFL7046;

DT 12-FEB-2004 (first entry)

XX Human albumin fusion protein-related protein SeqID2177.

XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.

XX Homo sapiens.

XX WO2003060071-A2.

XX 24-JUL-2003.

XX 23-DEC-2002; 2002WO-US040891.

XX 21-DEC-2001; 2001US-0341811P.

XX 24-JAN-2002; 2002US-0350358P.

XX 28-JAN-2002; 2002US-0351360P.

XX 26-FEB-2002; 2002US-0359370P.

XX 28-FEB-2002; 2002US-0360000P.

XX 27-MAR-2002; 2002US-0367500P.

XX 08-APR-2002; 2002US-0370227P.

XX 10-MAY-2002; 2002US-0378950P.

PR 24-MAY-2002; 2002US-0382617P.
 PR 28-MAY-2002; 2002US-0383123P.
 PR 03-JUN-2002; 2002US-0385708P.
 PR 10-JUL-2002; 2002US-0394625P.
 PR 24-JUL-2002; 2002US-0398008P.
 PR 09-AUG-2002; 2002US-0402131P.
 PR 13-AUG-2002; 2002US-0402708P.
 PR 18-SEP-2002; 2002US-0411355P.
 PR 18-SEP-2002; 2002US-0411426P.
 PR 02-OCT-2002; 2002US-0414984P.
 PR 11-OCT-2002; 2002US-0417611P.
 PR 23-OCT-2002; 2002US-0420246P.
 PR 05-NOV-2002; 2002US-0423623P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.
 PA (PRIN-) PRINCIPIA PHARM CORP.
 XX
 PI Balance DJ, Turner AJ, Rosen CA, Haseltine WA;
 DR WPI; 2003-598517/56.
 DR N-PSDB; ADP17040.
 XX
 PT New albumin fusion protein, useful for preparing a composition for
 PT treating diabetes mellitus.
 XX
 PS Example 4; SEQ ID NO 2177; 24pp; English.
 PS
 CC This invention relates to a novel albumin fusion protein having albumin
 CC or biological activity. Human serum albumin is responsible for a
 CC significant proportion of the osmotic pressure of serum and also
 CC functions as a carrier of endogenous and exogenous ligands. The fusion of
 CC albumin to a therapeutic protein may increase shelf-life and stability of
 CC the therapeutic protein. The albumin fusion protein of the invention may
 CC allow production of compositions with antidiabetic activity whilst the
 CC nucleotide sequence which encodes it may be useful for gene therapy. The
 CC albumin fusion protein is useful for preparing a composition for treating
 CC diabetes mellitus. The present sequence is that of a therapeutic protein
 CC which was fused with human albumin to create a novel albumin fusion
 CC protein of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/publishedpat_sequences
 XX
 SQ Sequence 162 AA;
 Query Match 100.0%; Score 850; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KM tumour progression; metastasis; tumour stasis; haematopoietic tumour;
 KM lymphoma; B cell tumour; systemic lupus erythematosus;
 KM rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;
 KM immunocompromised patient; HIV infection; vaccine; chromosome 4q27.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..31
 FT Protein /note="Signal peptide"
 FT /note="32..162
 FT /note="Mature Zalphall, claimed in claim 1"
 XX
 PN US6605272-B2.
 PD 12-AUG-2003.
 XX
 PF 03-AUG-2001; 2001US-00923246.
 XX
 PR 09-MAR-1999; 99US-0123547P.
 PR 11-MAR-1999; 99US-0123904P.
 PR 01-JUL-1999; 99US-0142013P.
 PR 09-MAR-2000; 2000US-00522217.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 PI Grosse JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX
 DR WPI; 2003-895283/82.
 XX
 PT Stimulating an immune response in a mammal exposed to an antigen or
 PT pathogen, useful for enhancing anti-tumor activity resulting in reduced
 PT tumor progression or metastasis, comprises administering zalphall ligand
 PT polypeptide.
 XX
 PS Claim 1; SEQ ID NO 2; 103pp; English.
 PS
 CC The invention relates to stimulating an immune response in a mammal
 CC exposed to an antigen or pathogen comprising administering a composition
 CC comprising mature zalphall ligand polypeptide comprising residues 32-162
 CC of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an
 CC immune response in a mammal exposed to an antigen or pathogen
 CC (comprising: (a) determining (in)directly the level of antigen or
 CC pathogen present in the mammal; (b) administering a composition
 CC comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c)
 CC determining (in)directly the level of antigen or pathogen in the mammal;
 CC and (d) comparing the antigen or pathogen level in (a) with (b), where a
 CC change in the level indicates stimulation of immune response), and
 CC stimulating an immune response in a mammal exposed to an antigen or
 CC pathogen (comprising: (a) determining a level of antigen- or pathogen-
 CC specific antibody; (b) administering a composition comprising zalphall
 CC ligand polypeptide in a pharmaceutical vehicle; (c) determining a post
 CC administration level in the antigen- or pathogen-specific antibody; and
 CC (d) comparing the level of the antibody in (a) with (b), where an
 CC increase in the antibody level indicates stimulation of immune response).
 CC The method is useful for stimulating an immune response in a mammal
 CC exposed to an antigen or pathogen, and for enhancing anti-tumor activity
 CC resulting in a reduction in tumour progression, decrease in metastasis,
 CC or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma
 CC or a B cell tumour. The zalphall ligand is useful for treating a wide
 CC range of diseases arising from defects in the immune system, e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or
 CC diabetes, for boosting immunity to infectious diseases, treating
 CC immunocompromised patients, such as HIV+ patients and in improving
 CC vaccines. The present sequence is a human zalphall ligand protein.
 XX
 SQ Sequence 162 AA;
 Query Match 100.0%; Score 850; DB 7; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNERRIIVNSIKKLKRKPPSTNAGROKRL 120
 DB 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNERRIIVNSIKKLKRKPPSTNAGROKRL 120
 QY 121 TCPSCDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 RESULT 12
 ADJ25621
 ID ADJ25621 standard; protein; 162 AA.
 AC ADJ25621;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 XX Human interleukin 21 (IL-21) protein SEQ ID NO:2.
 XX
 XX Interferon gamma inhibition; IFNgamma inhibition; interleukin 21 agonist;
 KM IL-21 agonist; antiaesthetic; antiallergic; antiarthritic; antirheumatic;
 KM neuroprotective; antiinflammatory; dermatological; immunosuppressive;
 KM muscular; antipneumatic; T helper; Th1; Th2; asthma; allergy;
 KM rheumatoid arthritis; multiple sclerosis; lupus; diabetes;
 KM Crohn's disease; psoriasis; myasthenia gravis; human; IL-21.
 XX
 OS Homo sapiens.
 XX
 PN WO2004007682-A2.
 XX
 PD 22-JAN-2004.
 XX
 PF 15-JUL-2003; 2003WO-US021975.
 XX
 XX 15-JUL-2002; 2002US-0396160P.
 PR 12-AUG-2002; 2002US-0403001P.
 XX
 PA (AMHP) WYETH.
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Grusby M, Wurster A, Young DA, Collins M, Walters MJ;
 XX
 DR WPI: 2004-1122921/12.
 XX
 DR N-PSDB: ADJ25620.
 XX
 XX Inhibiting interferon gamma (IFNgamma) levels and T helper cell
 PT development and function in a T cell or cell population using IL-21
 PT modulators, useful for the preventing and/or treating asthma, allergy,
 PT arthritis, lupus and diabetes.
 XX
 PS Claim 1; SEQ ID NO 2; 59pp; English.
 XX
 CC The present invention describes a method for inhibiting interferon gamma
 CC (IFNgamma) levels in a T cell population by contacting the T cell or cell
 CC population with an interleukin 21 (IL-21) agonist in an amount sufficient
 CC to inhibit IFNgamma in the T cell or cell population, wherein the agonist
 CC is an IL-21 polypeptide comprising an amino acid sequence at least 85%
 CC identical to the 162 amino acids (Seq ID NO: 2; ADJ25621), and which is
 CC capable of binding to an IL-21R. An IL-21 agonist has antiaesthetic,
 CC antiallergic, antiarthritic, antirheumatic, neuroprotective,
 CC antiinflammatory, dermatological, immunosuppressive, muscular and
 CC antipneumatic activities. The methods and compositions of the present
 CC invention are useful for the diagnosis, prevention and/or treatment of
 CC diseases or conditions associated with aberrant expression or activity of
 CC IL-21, T helper 1 (Th1) and/or Th2, such as asthma, allergy, rheumatoid
 CC arthritis, multiple sclerosis, lupus, diabetes, Crohn's disease,
 CC psoriasis and myasthenia gravis. The present sequence represents human IL
 CC -21, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 162 AA;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSSPGMERIVCLAWIFIGTLVHKSSSGODRHMRMQLDIVDOLKNYVNDLVPEF 60
 DB 1 MRSSPGMERIVCLAWIFIGTLVHKSSSGODRHMRMQLDIVDOLKNYVNDLVPEF 60
 QY 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNERRIIVNSIKKLKRKPPSTNAGROKRL 120
 DB 61 LPAPEDVETNCESAFSCFOKAOLKSANTGNERRIIVNSIKKLKRKPPSTNAGROKRL 120
 QY 121 TCPSCDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 DB 121 TCPSCDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
 RESULT 13
 ADM41017
 ID ADM41017 standard; protein; 162 AA.
 AC ADM41017;
 XX
 XX 15-JUL-2004 (first entry)
 DT
 XX
 DE Human IL-21 amino acid sequence, seq id 2.
 XX
 KM Antiallergic; antiaesthetic; antiparasitic; antiinflammatory;
 KM antihelminthic; dermatological; immunomodulatory; interleukin; IL-21;
 KM eosinophil; allergic; parasitic; asthma; allergic rhinitis;
 KM helminthic infection.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 30..162
 FT /note="region specifically referred to in claims"
 PN WO2004032953-A1.
 XX
 PD 22-APR-2004.
 XX
 PF 13-OCT-2003; 2003WO-DK000691.
 XX
 XX 11-OCT-2002; 2002DK-00001546.
 PR 16-OCT-2002; 2002DK-00001587.
 PR 17-OCT-2002; 2002US-0419225P.
 XX
 PA (NOVO) NOVO NORDISK AS.
 PA
 PI Romer J, Moller NPH, Skak K;
 XX
 DR WPI: 2004-340821/31.
 XX
 XX Use of Interleukin-21 for the treatment of diseases or conditions where
 PT eosinophils are involved in a protective response in a subject, e.g.
 PT allergic conditions and/or parasitic diseases.
 XX
 PS Claim 6; SEQ ID NO 2; 32pp; English.
 XX
 CC The invention relates to an interleukin (IL)-21 that is used for the
 CC treatment of diseases or conditions where eosinophils are involved in a
 CC protective response in a subject, e.g. allergic conditions and/or
 CC parasitic diseases. Methods of the invention are involved in a protective
 CC response in a subject, such as allergic conditions (e.g. asthma, allergic
 CC rhinitis or allergic diseases of the skin) and/or parasitic diseases,
 CC especially helminthic infection. The current sequence represents the DNA
 CC sequence encoding IL-21. Note: This sequence is not encoded by that of
 CC ADM41016, which we are told in the specification is the IL-21 encoding
 CC nucleotide.
 XX
 SQ Sequence 162 AA;

Query Match 100.0%; Score 850; DB 8; Length 162;
 Best Local Similarity 100.0%; Pred. No. 2e-86;

Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSSPGNMERIVICLMTVIFGLTVLHKSSSGQODRHMRMQLIDIVDLKXNVNDLVEF 60
Db 1 MRSSPGNMERIVICLMTVIFGLTVLHKSSSGQODRHMRMQLIDIVDLKXNVNDLVEF 60
Qy 61 LPAPEDVETNCENAFSCFOKAOLKSANTGNNERIINVISIKLKRKPPSTNAGRQKRL 120
Db 61 LPAPEDVETNCENAFSCFOKAOLKSANTGNNERIINVISIKLKRKPPSTNAGRQKRL 120
Qy 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 14
ADP12563
ID ADP12563 standard; protein; 162 AA.

AC ADP12563;
DT 12-AUG-2004 (first entry)

DE Protein encoded by mRNA of the invention #173.

XX transplamt rejection; immune system; rheumatoid arthritis; lupus;
KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS.

OS Homo sapiens.

XX MO2004042346-A2.

XX 21-MAY-2004.

XX 24-APR-2003; 2003WO-US012946.

XX 24-APR-2002; 2002US-00131831.

XX 20-DEC-2002; 2002US-00325899.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;

DR WPI; 2004-400724/37.

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.

XX Claim 65; SEQ ID NO 2572; 1762pp; English.

CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.

XX Sequence 162 AA;

Query Match 100.0%; Score 850; DB 8; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSSPGNMERIVICLMTVIFGLTVLHKSSSGQODRHMRMQLIDIVDLKXNVNDLVEF 60
Db 1 MRSSPGNMERIVICLMTVIFGLTVLHKSSSGQODRHMRMQLIDIVDLKXNVNDLVEF 60
Qy 61 LPAPEDVETNCENAFSCFOKAOLKSANTGNNERIINVISIKLKRKPPSTNAGRQKRL 120
Db 61 LPAPEDVETNCENAFSCFOKAOLKSANTGNNERIINVISIKLKRKPPSTNAGRQKRL 120
Qy 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 15
ADP19731
ID ADP19731 standard; protein; 162 AA.

AC ADP19731;

DT 26-AUG-2004 (first entry)

DE Human zalphall ligand.

XX cyrostatic; zalphall ligand; pharmaceutical; cancer; immune response;
KM melanoma; tumour; solid tumour; haematopoietic tumour; lymphoma; human;
KM chromosome 4.

OS Homo sapiens.

XX US2004110932-A1.

XX 10-JUN-2004.

XX 10-SEP-2003; 2003US-00659684.

XX 09-MAR-1999; 99US-0123547P.

XX 11-MAR-1999; 99US-0123904P.

XX 01-JUL-1999; 99US-0142013P.

XX 09-MAR-2000; 2000US-00522217.

XX (ZYMO) ZYMOGENETICS INC.

PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

DR WPI; 2004-440401/41.

PT New zalphall ligand polynucleotide and polypeptide molecules, useful for
PT treating cancer, e.g. melanoma, solid tumor, hematopoietic tumor, or
PT lymphoma.

XX Claim 1; SEQ ID NO 2; 111pp; English.

CC The invention describes an isolated polypeptide comprising a sequence of
CC amino acid residues that is at least 90 or 95% identical to residues 41
CC (Gln) to 148 (Ile), or 32 (Gln) to 148 (Ile) of a sequence of 162 amino
CC acids (SEQ ID NO:2, human zalphall ligand), fully defined in the
CC specification. Also described are: a pharmaceutical composition
CC comprising the polypeptide, and a vehicle; a method of creating cancer in
CC a mammal; a method of stimulating an immune response in a mammal with
CC melanoma; a method of stimulating an immune response in a mammal bearing
CC a tumour; an isolated polynucleotide comprising a sequence of nucleotides
CC that encode amino acid residues cited above, where the polynucleotide
CC encodes a polypeptide that binds a receptor comprising 538 amino acids,
CC fully defined in the specification; a pharmaceutical composition
CC comprising the polynucleotide encoding, in a pharmaceutically acceptable
CC vehicle; an expression vector comprising the following operably linked
CC elements a control element; and a DNA segment comprising the
CC polynucleotide; and an isolated polynucleotide molecule comprising at
CC least 10 nucleotides of the polynucleotide sequence of 642 bp, fully
CC defined in the specification. The molecules, compositions and methods are

CC useful for treating cancer, e.g. melanoma, solid tumour, haematopoietic
 CC tumour, or lymphoma. This is the amino acid sequence of novel human
 CC cytokine zaiphal1 ligand.

XX
 SQ Sequence 162 AA;

Query Match 100.0%; Score 850; DB 8; Length 162;

Best Local Similarity 100.0%; Pred. No. 2e-86;
 Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRSSPGNMRIVICLWYIFLGTLVHKSSSGODRHMIRMQLIDIVDQKNYVNDLVPEF	60
Db	1	MRSSPGNMRIVICLWYIFLGTLVHKSSSGODRHMIRMQLIDIVDQKNYVNDLVPEF	60
QY	61	LPAPEDVETNCWAFSCFOAKOLKSANTGNNRIINVSITKLRKPPSTNAGRROKRL	120
Db	61	LPAPEDVETNCWAFSCFOAKOLKSANTGNNRIINVSITKLRKPPSTNAGRROKRL	120
QY	121	TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSSTHGSSEDS	162
Db	121	TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSSTHGSSEDS	162

Search completed: September 7, 2006, 12:44:57
 Job time : 69.1143 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:45:21 ; Search time 11.8029 Seconds
(without alignments)
1320.622 Million cell updates/sec

Title: US-10-659-684-2
Perfect score: 850
Sequence: 1 MRSSPGMERIVICLAWIFL.....LLOQMTHQHSRRHSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.80.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.5	11.1	162	1 A53484	interleukin-15 pre
2	91.5	10.8	567	2 S29498	lymphocyte antigen
3	83	9.8	899	2 B38529	nkB protein - Bsc
4	82	9.6	607	1 ABX172	74k albumin precu
5	79	9.3	206	2 S49862	hypothetical prote
6	78	9.0	741	2 JC7822	isocitrate dehydro
7	76.5	9.0	420	2 A25876	vitellogenin III p
8	76.5	9.0	864	2 S60441	hypothetical prote
9	76	8.9	195	2 S42022	ureidoglycolate hy
10	75.5	8.9	336	2 S42632	Flt-15 protein pre
11	75.5	8.9	406	2 T28957	hypothetical prote
12	75.5	8.9	1206	2 S24407	formin isoform IV
13	75	8.8	321	2 T46352	hypothetical prote
14	74.5	8.8	286	2 F82881	hypothetical prote
15	74.5	8.8	482	2 S41211	voltage-dependent
16	74.5	8.8	789	2 S44759	ClAB9.5 protein -
17	74.5	8.8	440	2 T00372	hypothetical prote
18	74	8.7	440	2 T47906	FUSCA PROTEIN FUS6
19	74	8.7	953	2 I48078	CHO1 antigen - Chi
20	74	8.7	2197	2 B71600	variant-specific s
21	73.5	8.6	162	2 S49124	interleukin-15 - m
22	73.5	8.6	447	2 S39316	Ca2b protein - hu
23	73.5	8.6	472	2 T59087	ISG-K54 - human
24	73.5	8.6	477	2 S21049	calcium channel pr
25	73.5	8.6	484	2 S39315	CAB3a protein - hu
26	73.5	8.6	484	2 A46608	voltage-dependent
27	73.5	8.6	565	2 G89878	conserved hypotet
28	73.5	8.6	868	2 T31527	hypothetical prote
29	73.5	8.6	2118	2 T13612	hypothetical prote

30	73	8.6	234	2 G97966	hypothetical prote
31	73	8.6	304	2 A32108	translational initia
32	73	8.6	1291	2 T22382	hypothetical prote
33	72.5	8.5	309	2 T41889	P53 orf153 - Bomb
34	72.5	8.5	380	2 T25454	hypothetical prote
35	72.5	8.5	667	2 D96923	uncharacterized co
36	72.5	8.5	1101	2 T26919	hypothetical prote
37	72	8.5	257	2 C69230	conserved hypotet
38	72	8.5	262	2 F72858	probable methyl tr
39	72	8.5	262	2 T41813	AcMNPV orf69 - Bom
40	72	8.5	546	2 G72210	hypothetical prote
41	72	8.5	719	2 T27977	lin-15A protein -
42	72	8.5	990	2 T43445	hypothetical prote
43	71.5	8.4	421	2 C84555	hypothetical prote
44	71.5	8.4	484	2 S62185	calcium channel be
45	71.5	8.4	674	2 S61181	hypothetical prote

ALIGNMENTS

```

RESULT 1
A53484
interleukin-15 precursor - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A53484
R:Grabstein, K.H.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.; Bee
; Girt, J.G.
Science 264, 965-968, 1994
A:Title: Cloning of a T cell growth factor that interacts with the beta chain of the int
A:Reference number: A53484; MUID:94233380; PMID:8178155
A:Accession: A53484
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-162 <GBA>
A:Cross-references: UNIPROT:P40221; UNIPARC:UPI0000031AC6; GB:U03099; NID:9493521; PIDN:
F:49-162/Product: interleukin-15 #status predicted <MAR>
F:83-133,90-136/Disulfide bonds: #status predicted
Query Match 11.1%; Score 94.5; DB 1; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.19; 48; Indels 15; Gaps 5;
Matches 30; Conservative 23; Mismatches 25
Cy 43 IDIVDQKXNVNDLVPEF-----LPAPDEVETNCMSAFSCF---QKALKSANTGNNE 93
Db 51 VNVISDLKK-IEDILQSMHIDATLYTESDVHPSCKVTAMKCFLELVISHESGDTIHD 109
Cy 94 RIINVSIRKLRKRPSTNAGRRQRRLTSPSCDSYEKKPKPEFLERFKSLQKMH 149
Db 110 TVENLII--LANNLSSNGNITES---GCKECSELEENIKRIFQSFVHYQWFIN 160

RESULT 2
S29498
lymphocyte antigen ly84 precursor - mouse
N:Alternate names: 38.5K T1 glycoprotein; ST2L protein
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S29498; A33541; S17657; S07054
R:Yanagisawa, K.; Takagi, T.; Tanukamo, T.; Tetsuka, T.; Tomioka, S.
FEBS Lett. 318, 83-87, 1993
A:Title: Presence of a novel primary response gene ST2L, encoding a product highly simi
A:Reference number: S29498; MUID:93170492; PMID:7916701
A:Accession: S29498
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-567 <YAN>
A:Cross-references: UNIPROT:P14719; UNIPARC:UPI0000029617; EMBL:D13695; NID:9286100; PID
R:Klemenz, R.; Hoffmann, S.; Werenkiold, A.K.

```

[illegible]

```

Oy      34 Conservative    22; Mismatches 55; Indels 40; Gaps 7;
Db      38 SSSGCGDHHMTRMROLIDIVDLQKYYVNDLVEFLPAPEDVTNCWSAFA----SCGOKAQ 83
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Oy      38 SSSQAEQHRSRFSRLVDYATRLRN-----ESFVALVDVKDCGWNVFGVTCFNCT 91
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      84 LKSANTGNRRIRINVSIKKKRPSTNAGROKRKL---TCP-----SCSYEKPKPK 134
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy      92 SLFTAADMEIT-----ARQAHYAKDDTPRVFYIILSMQSHSHPRE 133
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      135 EFLERFKSLLOKM---IHQLSSRTGSEDS 162
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
        134 QYDSVRHTLKSLGLADHQVSA-VHPTDN 163
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
ABXL72
7AK albumin precursor - African clawed frog
C.Species: Xenopus laevis (African clawed frog)
C.Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #ext_change 09-Jul-2004
C.Accession: B41682; S02693; A05288
R.Moskatis, J.E.; Sargent, T.D.; Smith Jr., L.H.; Pastori, R.L.; Schenberger, D.R.
Mol. Endocrinol. 3, 464-473, 1989
A.Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic acid during development.
A.Reference number: A41682; MUID:89313788; PMID:2747653
A.Accession: B41682
A.Molecule type: mRNA
A.Residues: 3-607 <MO>
A.Cross-references: UNIPROT:P48472; UNIPARC:UPI00001714FB; GB:M21442; NID:g233930; PIDN:j
R.Schorp, M.; Doebeiling, U.; Wagner, U.; Ryffel, G.U.
J. Mol. Biol. 199, 83-93, 1986
A>Title: 5'-flanking and 5'-proximal exon regions of the two Xenopus albumin genes. Delet
A.Reference number: S02692; MUID:88172470; PMID:2451026
A.Accession: S02692
A>Status: not compared with conceptual translation
A.Molecule type: DNA
A.Residues: 1-48 <SCH>
A.Cross-references: UNIPARC:UPI000017441B; EMBL:226826
R.Wolffe, A.P.; Glover, J.F.; Martin, S.C.; Tennilwood, M.P.R.; Williams, J.L.; Tate, J.F.
Eur. J. Biochem. 146, 489-496, 1985
A>Title: Deduction of transcription of Xenopus 74-kDa albumin genes and destabilizator
A.Reference number: A05288; MUID:85126974; PMID:3971963
A.Accession: A05288
A.Molecule type: mRNA
A.Residues: 459-502, 'U', 504-557 <WOL>
A.Cross-references: UNIPARC:UPI000017441F; GB:M28276
A.Note: The authors translated the codon TAT for residue 63 as Thr
C.Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, iron
mones (weak bonds with these hormones promote their transfer across the membranes), thyroxine
C.Genetics:
A.Introns: 27/1
C.Subfamily: serum albumin, serum albumin repeat homology
C.Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma
F.1-18/Domin: signal sequence #status predicted <SIG>
F.19-24/Domin: propeptide #status predicted <PRO>
F.25-607/Product: 74K serum albumin #status predicted <MAT>
F.32-201/Domin: serum albumin repeat homology <SA1>
F.220-393/Domin: serum albumin repeat homology <SA2>
F.412-591/Domin: serum albumin repeat homology <SA3>
F.30/Binding site: copper (His) #status predicted
F.80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-392,'
F.256/Binding site: carbohydrate (Asn) (covariant) #status predicted

Query Match          9.6%; Score 82; DB 1; Length 607;
Best Local Similarity 24.2%; Pred. No. 11;
Matches   38; Conservative 19; Mismatches 50; Indels 50; Gaps 6;

Oy      44 DIVDLQKYYVNDLVEFLPAPEDVTNCWSAFAFCF---QKAQLKSAN 88
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      72 EINPFAKSCINDKTPECEKPVGTLEFDKLCADPAVGWNVSWSKCCAKODPERAQCFKAH 131
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy      89 TGNNERRI---NWSIKKLKRC-----PPSTNAGRGRGHRLTSPS 124

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Db 132 RDHNTSIKPEPEETCKLKHPPDLLSATFHESARHNPDIYPAYVALTRQYHKLAEHC 191
 Qy 125 CDSYEKKPKPEFLERFKSLLOKMIHOLISRTGSED 161
 Db 192 CEEEDKE--KCFSEKMKQLMK-----QSHSIED 217

RESULT 5

S49882
 hypothetical protein YII127C - Yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein YI8277.02c
 C/Species: Saccharomyces cerevisiae
 C/Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C/Accession: S49882
 R/Hamlyn, N.; Church, C.
 submitted to the EMBL Data Library, November 1994
 A/Reference number: S49881
 A/Accession: S49882
 A/Molecule type: DNA
 A/Residues: 1-206 <HAM>
 A/Cross-references: UNIPROT:P40470; UNIPARC:UPI000013B441; GB:Z47047; EMBL:Z46833; NID:G
 C/Genetics:
 A:Gene: MIPS:YII127C
 A/Cross-references: SGD:S0001389
 A/Map position: 9L

Query Match 9.3%; Score 79; DB 2; Length 206;
 Best Local Similarity 26.1%; Pred. No. 6.4;
 Matches 29; Conservative 18; Mismatches 48; Indels 16; Gaps 3;

Qy 48 QLNKYVNDLVEFLPAPEDVTNCMSAFSCFOQAOLKSANTGNRRINVSICKLRKP 107
 Db 12 QATSVVNGLLSNLPGPKIRANNKTSVNGSKAOLIDRLKKRVQLOQNRDVHKIKKCC 71

Qy 108 PSTNAGRRORHRLTSPSCDSYEKKPKPEFLERF--KSLLOKMIHOLISRT 156
 Db 72 KLVKKKKVKQKHL-----DKQEQSLAKHGVLRK--HGHGTLT 108

RESULT 6

JC7822
 isocitrate dehydrogenase (NADP) (EC 1.1.1.42), monomeric type - Azotobacter vinelandii
 C/Species: Azotobacter vinelandii
 C/Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004
 C/Accession: JC7822; PC7187
 R/Sahara, T.; Takeuchi, Y.; Yamaoka, N.; Fukunaga, N.
 Bioccl. Biotechnol. Biochem. 66, 489-500, 2002
 A/Title: Cloning, sequencing, and expression of a gene encoding the monomeric isocitrate
 A/Reference number: JC7822; PMID:12005040; MUID:21999801
 A/Accession: JC7822
 A/Molecule type: DNA
 A/Residues: 1-741 <SAH>
 A/Cross-references: UNIPROT:P16100; UNIPARC:UPI000012D1CA; DDBJ:D73443
 A/Accession: PC7187
 A/Molecule type: Protein
 A/Residues: 2-16 <SA2>
 C/Species: Saccharomyces cerevisiae
 C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
 C/Accession: S60441; S64459
 R/Skala, J.; Nawrocki, A.; Goffeau, A.
 Yeast 11, 1421-1427, 1995
 A/Title: The sequence of a 27 kb segment on the right arm of chromosome VII from Sacchar
 A/Reference number: S60435; MUID:96158062; PMID:8585325
 A/Accession: S60441
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-864 <SA>
 A/Cross-references: UNIPROT:P48237; UNIPARC:UPI000005309F; EMBL:X85807; NID:g1045249; PI
 R/Van Dyck, L.; Skala, J.; de Wierfossse, P.; Purnelle, B.; Talla, E.; Nawrocki, A.; Del
 submitted to the Protein Sequence Database, May 1996
 A/Reference number: S64428
 A/Accession: S64459

Query Match 9.2%; Score 78; DB 2; Length 741;
 Best Local Similarity 24.8%; Pred. No. 31;
 Matches 26; Conservative 23; Mismatches 34; Indels 22; Gaps 4;

Qy 33 DRHMRKRLIDIVDQKNYVNDL-----VPEFLPAPEDVTNCMSAFSCFOQAOLKS 86
 Db 77 DANIKKPNISASVPLKAKKEIQGQCYKLPD---PEEKPTDEKDVKARYKIKGSA 133

Qy 87 AN-----TGNNRRINVSICKLRKPSTNAGRRORHRLTSPSCDS 127
 Db 134 VNPVLRGNSDRRAPLSVKYARKHP-----HGMGWSADS 169

RESULT 7

A25876
 vitellogenin III precursor - fruit fly (Drosophila melanogaster)
 N/Alternate names: yolk polypeptide yP11; yolk protein 3
 C/Species: Drosophila melanogaster
 C/Date: 04-Mar-1988 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
 C/Accession: A25876; A27388
 R/Yan, Y.L.; Kunert, C.J.; Postlethwait, J.H.
 Nucleic Acids Res. 15, 67-85, 1987
 A/Title: Sequence homologies among the three yolk polypeptide (Yp) genes in Drosophila m
 A/Reference number: A25876; MUID:87146365; PMID:3029679
 A/Accession: A25876
 A/Molecule type: DNA
 A/Residues: 1-420 <YAN>
 A/Cross-references: UNIPROT:P06607; UNIPARC:UPI0000080099; GB:X04754; NID:g8844; PIDN:CA
 R/Garabedian, M.J.; Shitras, A.D.; Bowmer, M.; Wensink, P.C.
 Gene 55, 1-8, 1987
 A/Title: The nucleotide sequence of the gene coding for Drosophila melanogaster yolk pro
 A/Reference number: A27388; MUID:87305580; PMID:3114046
 A/Accession: A27388
 A/Molecule type: DNA
 A/Residues: 1-420 <GAR>
 A/Cross-references: UNIPARC:UPI0000080099; GB:M15898; NID:g158815; PIDN:AAA29024.1; PID:
 C/Genetics:
 A:Gene: FlyBase:Yp3
 A/Cross-references: FlyBase:FBgn0004047
 C/Superfamily: Insect vitellogenin
 C/Keywords: egg yolk; glycoprotein; phosphoprotein; sulfoliprotein
 F.1-19/Domain: signal sequence #status predicted <SIG>

Query Match 9.0%; Score 76.5; DB 2; Length 420;
 Best Local Similarity 24.4%; Pred. No. 23;
 Matches 39; Conservative 14; Mismatches 54; Indels 53; Gaps 7;

Qy 8 MERIVCLMWIFLGTIVHKSSSGQDR-----HMIRROLIDI----- 45
 Db 1 MMSLRICLAVTCLVAHASKDASNDRLKPTKMLTATELEVPISLNDITERLENOPLAQ 60

Qy 46 -----VDQKNYVNDLVEFLPAPEDVTNCMSAFSCFOQAOLK-----SA 87
 Db 61 GAKYIEKIVYVGQIK--HDLTSPFVSPSNVPV--WIKSNQKVECKLNNYETAKA 114

Qy 88 NTGNNRRINVSICKL--KRPSTNAGR-----OKHRL 120
 Db 115 QPFGEDVETIVLTGLFKTSPAQKARRLLQAYVQKYNL 154

RESULT 8

S60441
 hypothetical protein YGR150C - Yeast (Saccharomyces cerevisiae)
 N/Alternate names: hypothetical protein G6642
 C/Species: Saccharomyces cerevisiae
 C/Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
 C/Accession: S60441; S64459
 R/Skala, J.; Nawrocki, A.; Goffeau, A.
 Yeast 11, 1421-1427, 1995
 A/Title: The sequence of a 27 kb segment on the right arm of chromosome VII from Sacchar
 A/Reference number: S60435; MUID:96158062; PMID:8585325
 A/Accession: S60441
 A/Status: nucleic acid sequence not shown
 A/Molecule type: DNA
 A/Residues: 1-864 <SA>
 A/Cross-references: UNIPROT:P48237; UNIPARC:UPI000005309F; EMBL:X85807; NID:g1045249; PI
 R/Van Dyck, L.; Skala, J.; de Wierfossse, P.; Purnelle, B.; Talla, E.; Nawrocki, A.; Del
 submitted to the Protein Sequence Database, May 1996
 A/Reference number: S64428
 A/Accession: S64459

A:Molecule type: DNA
A:Residues: 1-864 <VAN>
A:Cross-references: UNIPARC:UPI000005309F, EMBL:Z72935, NID:g1323253, PIDN:CAA97164.1, F
A:Experimental source: strain S288C
C:Genetics:
A:Cross-references: SGD:S0003382
A:Map position: 7R

Query Match 9.0%; Score 76.5; DB 2; Length 864;
Best Local Similarity 22.5%; Pred. No. 49;

Matches 43; Conservative 22; Mismatches 59; Indels 67; Gaps 8;

QY 2 RSSPGRNERYIC---LMVFLGTLVHKSSQGDRIIMRQIDIVDQLKQVYNDLV 57
DB 5 RCGPKKN---VLCPPFQSLFSLKRLNK-----RFKYTLQTEDE-KMMWSLS 49
QY 58 PEFLPAPDEVETNCESAFSCFOKAOLKSANTGNMERIINVSIKLKRKPESTNAGRQK 117
DB 50 KKKITPEDEV-----FKLAQLREFSNTLKERIHNTK-----SVNSDGHQS 90
QY 118 HRLTSPSCDYEKKPK-----EFLERFKSLLOKMIHQ----- 150
DB 91 NSIAPISDESRNVVTVTSVSPNEEKSNIISDLIHSFLEKMDILVPRVIRVADDDIL 150
QY 151 --HSSRTGHS 159
DB 151 AKNLPDRSHSN 161

RESULT 9
S42022
ureidoglycolate hydrolase (EC 3.5.3.19) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YIR032C
C:Species: Saccharomyces cerevisiae
C:Date: 31-Mar-1992 #sequence_revision 14-Sep-1994 #text_change 05-Oct-2004
C:Accession: S42022; S48494
R:Yoc, H.S.; Cooper, T.G.
Yeast 7, 693-698, 1991

A:Title: The ureidoglycolate hydrolase (DAL3) gene in Saccharomyces cerevisiae.

A:Reference number: S42022; MUID:92133160; PMID:1776360

A:Accession: S42022

A:Molecule type: DNA

A:Residues: 1-195 <YOO>

A:Cross-references: UNIPROT:P32459, UNIPARC:UPI000005259B, EMBL:M64778; NID:g171369; PIR

R:Rowley, K.
submitted to the EMBL Data Library, October 1994

A:Reference number: S48494

A:Accession: S48494

A:Molecule type: DNA

A:Residues: 1-195 <ROW>

A:Cross-references: UNIPARC:UPI000005259B, GB:Z47047, EMBL:Z38061; NID:g603997; PID:g763

C:Genetics:
A:Gene: SGD:DAL3

A:Cross-references: SGD:S0001471; MIPS:YIR032C

A:Map position: 9R

C:Superfamily: ureidoglycolate hydrolase
C:Keywords: allantoin degradation; hydrolase; lipoprotein; methylated carboxyl end; pre-
F₁/F₂ binding site; larnesyl (Cys) (covalent) #status predicted
F₁/F₂/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match 8.9%; Score 76; DB 2; Length 195;
Best Local Similarity 27.6%; Pred. No. 11;
Matches 24; Conservative 14; Mismatches 29; Indels 20; Gaps 3;

QY 24 VHKSSQGDRIIMRQIDIVDQLKQVYNDLVPEFLPAPDEVETNCESAFSCFOKAQ 83
DB 33 LEKGANGGT---AIKLQ---VSQVENKSTSKVP-----NNMLPFCFQPH 72
QY 84 LKSANTGNMERIINVSIKLKRKPEST 110
DB 73 LNRVFTGSGNOAISHSIKVLEKHPGST 99

RESULT 10

S42632
Fit-1S protein precursor - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S42632

R:Bergers, G.; Reikhsatorfer, A.; Braselmann, S.; Graninger, P.; Bueslinger, M.

EMBO J. 13, 1176-1188, 1994

A:Title: Alternative promoter usage of the Fos-responsive gene Fit-1 generates mRNA isofo

A:Reference number: S42632; MUID:94178260; PMID:8131748

A:Accession: S42632

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-336 <BBR>

A:Cross-references: UNIPROT:Q62611; UNIPARC:UPI000002AC15; GB:U04319; NID:g488278; PIDN:J

C:Superfamily: vaccinia virus B15R protein; Immunoglobulin homology

Query Match 8.9%; Score 75.5; DB 2; Length 336;
Best Local Similarity 22.2%; Pred. No. 23;
Matches 30; Conservative 26; Mismatches 42; Indels 37; Gaps 6;
QY 43 IDIVDQLKQVYNDLV-----EFLPAPDEVETNCESAFSCFOKAOLKSAN 88
DB 49 INPEWYYSNTNERIPQKRNRIIVSRDLKFLPAKVE-----DSGIYTCVIRSP-ESIK 102
QY 89 TGNMERIINVSIKLKRKPE-----STNAGRQKRLTGPCSDSYEKKPKPEFLE 138
DB 103 TGS---LNVITLYK---RPNCKIPDYMYSTVDGSDKSKITCPTALYNMTAFVOMFK 155
QY 139 RPKSLQKMIHQHLS 153
DB 156 NCKALQGRPRRAHMS 170

RESULT 11
T28957
hypochemical protein F45F2.11 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28957

R:Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans csmid F45F2.

A:Reference number: Z20548

A:Accession: T28957

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-406 <DAV>

A:Cross-references: UNIPROT:Q22975; UNIPARC:UPI00000765A; EMBL:U64845; PIDN:AA48032.1;

A:Experimental source: strain Bristol N2; clone F45F2

C:Genetics:
A:Gene: CESP:F45F2.11

A:Map position: 5

A:Introns: 1/2; 24/2; 143/3; 307/2; 338/2

Query Match 8.9%; Score 75.5; DB 2; Length 406;
Best Local Similarity 20.5%; Pred. No. 28;
Matches 38; Conservative 23; Mismatches 55; Indels 69; Gaps 7;

QY 26 KSSSQGDRIIMRQIDIVDQLKQVYNDLVPEFLP-----SAFSCFOKAOLKSANTGNER 94
DB 13 KSSQSSDENFPRKLOQKRLRLK-----TEFLKESELEIEKNEKSGIOKCGENEG 66
QY 63 -----APDEVETNC----- 94
DB 67 ENEKCEFRPVVPNEIDSHKEWYHRLMLKLEYKGERGAPFPFPPPLPSMMIAASNA 126
QY 95 IINVSIKLKR-----KPESTNAGRQKRLTGPCSDSYEKKPKPEFLERFKSLQKM 147
DB 127 VSFNAFDEVRAAQAQAKTAKSPSTSLERRAQR-CPA-DFOPLPPPIIYTEMRTLAP-- 182
QY 148 IHOHL 152

Db 183 -HOXI 186

RESULT 12

S24407

formin isoform IV - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S24407

R:Jackson-Grusby, L.; Kuo, A.; Leder, P.

Genes Dev. 6, 29-37, 1992

A:Title: A variant limb deformity transcript expressed in the embryonic mouse limb defici

A:Reference number: S24407; MUID:92112033; PMID:1339380

A:Accession: S24407

A:Molecule type: mRNA

A:Residues: 1-1206 <AAC>

A:Cross-references: UNIPROT:Q05859; UNIPARC:UPI0000027920; EMBL:X62379; NID:g51552; PIDN

Query Match 8.8%; Score 75.5; DB 2; Length 1206;

Best Local Similarity 22.0%; Pred. No. 86;

Matches 37; Conservative 41; Mismatches 69; Indels 21; Gaps 8;

Qy 2 RSSPG--NMERI--VICLMVIFLGLVHKSSSGO--DHMIRMQLIDIVQLKVVY-- 54

Db 953 RASGLHMKSVKDIILALILFNGYMGNGNRTGQADGYSLEILPKLDVSRDNGMLV 1012

Qy 55 DLVEFLPAPDEVETNCESWAFSCFOKAQLKSANTGNNRIINVSIKKLKRPSTNAGR 114

Db 1013 DYVVKKYLYRYVDQEGAGTDSVPLPEPDQFLASQVKEFDLLK-DLRKLKQLEAS---- 1067

Qy 115 RQKRLTLCPSCDSEYKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Db 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

Qy 1068 EQQKMLVC-----KSPREYLOPFKDKLEFFPK--AKKEHKMEES 1106

RESULT 14

hypotheical protein U0505 (imported) - Ureaplasma urealyticum

C:Species: Ureaplasma urealyticum

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: F82881

R:Glass, J.I.; Letkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to Genbank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min

A:Reference number: A82870

A:Accession: F82881

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <GLA>

A:Cross-references: UNIPARC:UPI00000C1C9A; GB:AE002149; GB:AF222894; NID:g6899503; PIDN:

A:Experimental source: serovar 3; biovar 1

C:Genetics:

A:Gene: U0505

A:Genetic code: SGC3

Query Match 8.8%; Score 74.5; DB 2; Length 286;

Best Local Similarity 20.6%; Pred. No. 24;

Matches 42; Conservative 38; Mismatches 59; Indels 65; Gaps 9;

Qy 6 GNMERYICLMVIFLGLVHKSS-----SSQODRHMIMRQLIDIVD 47

Db 21 GGIISLIVITVAILIGVILSTONTNKSKEKPLTOIEDNINNKQDAH--KVNENITIID 78

Qy 48 QLK-----NVVN--DLVEFLPAPDEVETNCESWAFSCFOKAQLKSANTGNN 92

Db 79 KKGGIHKKIDITKINOQKEILKDYLNKKEK-----NKDQINNTNEYN 126

Qy 93 ERIINV-----SIKKLKRKPSTNAGRQKRLTSCDSYEKKPKPEFLERPKS 142

Db 127 KPIINVKVDDKNQKQENSTKLNNDPISNDKNK--INENNNI SYEEKPKPK--LKRENI 182

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Qy 143 L-----LOKMIHQHLSRTHGSEDS 162

Db 183 INVIAKKKDIYQLADFTYFSNEN 206

Thu Sep 7 14:13:59 2006

us-10-659-684-2.rpr

Page 6

Db 167 VPPYDVVPSMRPVVLVGPSLKGYE-----VTDMMQKALEDFLKHREFDG 209

Search completed: September 7, 2006, 12:52:26
Job time : 14.8029 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:40:11 ; Search time 89.3314 Seconds
(without alignments)
1677.489 Million cell updates/sec

Title: US-10-659-684-2
Perfect score: 850
Sequence: 1 MRSSPGMERIVICLWVIFL.....LLOKMIHQHLSRTGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniProt_sprotc:*
2: uniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813	95.6	155	1121_HUMAN	Q9bhe4 homo sapien
2	629	74.0	146	1121_BOVIN	Q761u5 bos taurus
3	609	71.6	146	1121_PIG	Q761u6 sus scrofa
4	604	71.1	146	1121_CANFA	Q6719 canis famli
5	486	57.2	146	1121_MOUSE	Q6e817 mus musculu
6	486	57.2	146	Q5SUE2_MOUSE	Q5ue22 mus musculu
7	392	46.1	123	1121_PERRA	Q80xg2 peromyscus
8	171.5	20.2	145	Q58106_CHICK	Q581u6 gallus gall
9	119.5	14.1	145	Q38121_TETNG	Q38121 tetradon n
10	106.5	12.5	162	1115_FELCA	Q97687 felis silve
11	99.5	11.7	135	Q6FGY7_HUMAN	Q6FGY7 homo sapien
12	99.5	11.7	162	1115_HUMAN	P40933 homo sapien
13	99.5	11.7	162	Q49528_HUMAN	Q49528 homo sapien
14	98.5	11.6	155	Q59902_FUGRU	Q59902 fugu rubrip
15	98.5	11.6	162	1115_RABIT	Q35942 oryctolagus
16	98	11.5	162	Q5W7F5_BRARE	Q5W7F5 brachydanio
17	96	11.3	160	Q32PM5_BRARE	Q32pm5 brachydanio
18	94.5	11.1	162	1115_CERRA	P40221 ceropithhec
19	94.5	11.1	162	1115_MACMU	P48092 macaca mula
20	94.5	11.1	162	Q4U002_MACTH	Q4U002 macaca thib
21	92	10.8	163	Q2PUG6_RABIT	Q2PUG6 oryctolagus
22	91.5	10.8	337	Q5D095_MOUSE	Q5D095 mus musculu
23	91.5	10.8	567	11R1L_MOUSE	P14719 mus musculu
24	91.5	10.8	567	Q3UM53_MOUSE	Q3um53 mus musculu
25	90.5	10.6	162	1115_BOVIN	Q28028 bos taurus
26	90.5	10.6	162	1115_SHEEP	Q93516 ovvis aries
27	89.5	10.5	162	Q75S29_CAVPO	Q75s29 canis porce
28	87.5	10.3	162	Q6B416_HORSE	Q6B416 equus cabal
29	86.5	10.2	162	Q5E8K6_MARMO	Q5e8k6 marmota mon
30	86.5	10.2	722	Q7MDK0_VIBVY	Q7mdk0 vibrio vuln
31	86	10.1	466	Q5C0J3_SCHUA	Q5c0j3 schistosoma

ALIGNMENTS

RESULT 1	ID	1121_HUMAN	STANDARD;	PRT;	155 AA.
AC	Q9HBE4				
DT	23-NOV-2004	integrated into UniProtKB/Swiss-Prot.			
DT	23-NOV-2004	Sequence version 2.			
DT	07-FEB-2006	entry version 24.			
DE	Interleukin-21 precursor (IL-21) (Za11).				
GN	Name=IL21;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.				
RK	MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;				Q5W7F6 brachydanio
RA	Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,				Q4GZL1_BUBBU
RA	Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,				Q5WQV8_MARMO
RA	Burkhead S., Heipel M., Brandt C., Kuilper J.L., Kramer J.,				Q42302_PLABE
RA	Conklin D., Pressnell S.R., Berry J., Shiota F., Bort S., Hamblit K.,				Q81913_LOXLA
RA	Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,				Q5A2U1_CANAL
RA	Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,				Q8D6P4_VIBVY
RA	Maurer M., Kaushansky K., Holly R.D., Foster D.,				Q4WQV6_ASFRU
RA	"Interleukin 21 and its receptor are involved in NK cell expansion and				Q8DUS6_SYNEU
RL	regulation of lymphocyte function.";				Q82933_9PORTV
RL	Nature 408:57-63 (2000).				Q7MNL4_VIBVY
RN	[2]				Q642P7_XENLA
RP	NUCLEOTIDE SEQUENCE (GENOMIC DNA).				Q4FIJ3_9ENR
RA	Rieder M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,				Q52336_ZZZZZ
RA	Nguyen D.A., Livingston R.J., Poel C.L., Nickerson P.D.,				
RA	Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;				
RT	"SeatlensNP, NHLBI H66682 program for genomic applications, UM-				
RT	PHRC, Seattle, WA (URL: http://pga.gs.washington.edu).";				
RT	Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stedileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udén T.B., Toehiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,				
RA	Bosak S.A., McEwan P.V., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Whaley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallue D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP FUNCTION.
RX PubMed=15178704; DOI=10.1189/jlb.1003488;
RA Strenge M., Julkunen I., Matikainen S.;
RT "IFN- α 1 α regulates IL-21 and IL-21R expression in human NK and T
RN cells.";
RN J. Leukoc. Biol. 76:416-422(2004).
RN [5]
RP REVIEW.
RX PubMed=15147560; DOI=10.1111/j.1365-2567.2004.01886.x;
RA Sivakumar P.V., Foster D.C., Clegg C.H.;
RT "Interleukin-21 is a T-helper cytokine that regulates humoral immunity
RT and cell-mediated anti-tumour responses.";
RL Immunology 112:177-182(2004).
CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
CC transition between innate and adaptive immunity. Induces the
CC production of IgG(1) and IgG(3) in B-cells (By similarity). May
CC play a role in proliferation and maturation of natural killer (NK)
CC cells in synergy with IL15. May regulate proliferation of mature
CC B- and T-cells in response to activating stimuli. In synergy with
CC IL15 and IL18 stimulates interferon gamma production in T-cells
CC and NK cells. During T-cell mediated immune response may inhibit
CC dendritic cells (DC) activation and maturation.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed in activated CD4-positive T-cells
CC but not in CD8-positive T-cells, B-cells, or monocytes.
CC -1- SIMILARITY: Belongs to the IL-21 family.
CC -----
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CC -----
DR EMBL: AF254069; AAC29348.1; ALT_INIT; mRNA.
DR EMBL: AY763518; AAU88182.1; ALT_INIT; mRNA.
DR EMBL: BC066258; AAH66258.1; ALT_INIT; mRNA.
DR EMBL: BC066259; AAH66259.1; ALT_INIT; mRNA.
DR EMBL: BC066260; AAH66260.1; ALT_INIT; mRNA.
DR EMBL: BC066261; AAH66261.1; ALT_INIT; mRNA.
DR EMBL: BC066262; AAH66262.1; ALT_INIT; mRNA.
DR EMBL: BC069124; AAH69124.1; ALT_INIT; mRNA.
DR EMBL: ENSG00000138664; Homo sapiens.
DR HGN: HGNC:6005; IL21.
DR MIM: 605384; gene.
DR GO: GO:0005615; C:extracellular space; NAS.
DR GO: GO:0005134; F:interleukin-2 receptor binding; IPI.
DR GO: GO:0048469; P:cell maturation; IDA.
DR GO: GO:0045078; P:positive regulation of interferon-gamma bio. .; NAS.
DR GO: GO:0042102; P:positive regulation of T cell proliferation; IDA.
DR GO: GO:0007165; P:signal transduction; NAS.
KM Cytokine; Glycoprotein; Signal.
FT CHAIN 1 22 Interleukin-21.
FT SIGNAL 23 155 Potential.
FT CARBOHYD 90 90 /FTID=PRO_0000015505.
FT DISULFID 64 115 N-linked (GlcNAc...) (Potential).
FT DISULFID 71 118 Potential.
SQ SEQUENCE 155 AA; 17923 MW; E994A3D19029B914 CRC64;
Query Match 95.6%; Score 813; DB 1; Length 155;
Best Local Similarity 100.0%; Pred. No. 1; ee-64;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128 YEKPPKEFLERFKSLQKMIHQHLSRTGSEDS 162
DB 121 YEKPPKEFLERFKSLQKMIHQHLSRTGSEDS 155
RESULT 2
ID IL21 BOVIN STANDARD; PRT; 146 AA.
AC Q76L05;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 23-NOV-2004, sequence version 2.
DT 07-FEB-2006, entry version 12.
DE Interleukin-21 precursor (IL-21).
GN Name:IL21;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], PROTEIN SEQUENCE OF 18-32, SUBCELLULAR
RP LOCATION, AND TISSUE SPECIFICITY.
RX PubMed=12969638; DOI=10.1016/S0165-2427(03)00106-5;
RA Muneta Y., Kikuma R., Yoshihara K., Mori Y.;
RT "Cloning, expression, and tissue distribution of bovine interleukin-
RT 21.";
RL Vet. Immunol. Immunopathol. 95:73-80(2003).
CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
CC transition between innate and adaptive immunity. Induces the
CC production of IgG(1) and IgG(3) in B-cells. May play a role in
CC proliferation and maturation of natural killer (NK) cells in
CC synergy with IL15. May regulate proliferation of mature B- and T-
CC cells in response to activating stimuli. In synergy with IL15 and
CC IL18 stimulates interferon gamma production in T-cells and NK
CC cells (By similarity). During T-cell mediated immune response may
CC inhibit dendritic cells (DC) activation and maturation (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed in spleen, but not in the brain,
CC heart, kidney, liver, and lung.
CC -1- SIMILARITY: Belongs to the IL-21 family.
CC -----
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CC -----
DR EMBL: AB073021; BAC87747.1; ALT_INIT; mRNA.
DR CYCLOKINE; Direct protein sequencing; Signal.
FT SIGNAL 1 17 Probable.
FT CHAIN 18 146 Interleukin-21.
FT DISULFID 64 115 /FTID=PRO_0000015503.
FT DISULFID 71 118 Potential.
SQ SEQUENCE 146 AA; 16948 MW; 696566DA73F4B8BC CRC64;
Query Match 74.0%; Score 629; DB 1; Length 146;
Best Local Similarity 81.5%; Pred. No. 4; ee-48;
Matches 119; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

OY 128 YEKPPKEFLERFKSLQKMIHQHLS 153
DB 121 YEKPPKEFLERFKSLQKMIHQHLS 146
RESULT 3

IL21_PIG STANDARD; PRT; 146 AA.
 ID IL21_PIG
 AC Q76LUG;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 23-NOV-2004, sequence version 2.
 DT 07-FEB-2006, entry version 12.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 OC Sus.
 NCBI_TaxID=96823;
 RX PubMed:15107555; DOI=10.1292/jvms.66.269;
 RA Muneta Y., Kikuma R., Uenishi H., Hoshino T., Yoshihara K., Tanaka M.,
 RA Hanashima N., Mori Y.,
 RT "Molecular cloning, expression and biological function of porcine
 RT interleukin-21."
 RL J. Vet. Med. Sci. 66:269-275(2004).
 CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC transition between innate and adaptive immunity. Induces the
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in
 CC proliferation and maturation of natural killer (NK) cells in
 CC synergy with IL15. May regulate proliferation of mature B- and T-
 CC cells in response to activating stimuli. In synergy with IL15 and
 CC IL18 stimulates interferon gamma production in T-cells and NK
 CC cells (By similarity). During T-cell mediated immune response may
 CC inhibit dendritic cells (DC) activation and maturation.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC
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 CC
 DR EMBL, AB073020; BAD11128.1; ALT_INIT; mRNA.
 KW Cytokine; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 146 Interleukin-21.
 FT DISULFID 64 115 /FTID=PRO_0000015508.
 FT DISULFID 71 118 Potential.
 SQ SEQUENCE 146 AA; 16833 MW; 835C63B716230BD1 CRC64;
 Query March 71.6%; Score 609; DB 1; Length 146;
 Best Local Similarity 80.1%; Pred. No. 2.7e-46;
 Matches 117; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
 QY 8 MERIVICIMVIFLGTLVHKSSSGQDRHIMRQLIDIVDQKNYVNDLVEFLPAPEDV 67
 DB 1 MEKIVICIMVIFSGTVAHKSSFGQDRLILRLQIDIVDQKNYVNDLPELPPAPEDV 60
 QY 68 ETNCEWSAFSCFOKAQLKSAANTGNRRINVSIKLKKRPSTNAGRRQKRLTSPSCDS 127
 DB 61 QRHCQSASFSCFOKVELKSAANTGNDEKLIINVLTKRKLPPTNAGRRQKRLTSPSCDS 120
 QY 128 YEKRPKEFLERFKSLQKMIHQHLS 153
 DB 121 YEKRPKEFLERFKSLQKMIHQHLS 146
 Db
 RESULT 4
 IL21_CANFA STANDARD; PRT; 146 AA.
 ID IL21_CANFA
 AC Q6L7I9;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 NCBI_TaxID=9615;
 RX NCI
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP TISSUE=Spleen;
 RC Miyake M., Saze K., Haga Y., Yamamoto Y., Iwabuchi S.,
 RA Submitted (DSC-2003) to the EMBL/Genbank/DBJ databases.
 RL "Molecular cloning of canine interleukin-21 cDNA."
 CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC transition between innate and adaptive immunity. Induces the
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in
 CC proliferation and maturation of natural killer (NK) cells in
 CC synergy with IL15. May regulate proliferation of mature B- and T-
 CC cells in response to activating stimuli. In synergy with IL15 and
 CC IL18 stimulates interferon gamma production in T-cells and NK
 CC cells (By similarity). During T-cell mediated immune response may
 CC inhibit dendritic cells (DC) activation and maturation (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC
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 CC
 DR EMBL, AB127975; BAD22569.1; - mRNA.
 DR Ensembl; ENSCAFG0000004004; Canis familiaris.
 KW Cytokine; Signal.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 146 Interleukin-21.
 FT DISULFID 64 115 /FTID=PRO_0000015504.
 FT DISULFID 71 118 Potential.
 SQ SEQUENCE 146 AA; 16776 MW; FFE8DF836AF219AA CRC64;
 Query March 71.1%; Score 604; DB 1; Length 146;
 Best Local Similarity 80.8%; Pred. No. 7.4e-46;
 Matches 118; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
 QY 8 MERIVICIMVIFLGTLVHKSSSGQDRHIMRQLIDIVDQKNYVNDLVEFLPAPEDV 67
 DB 1 MEKIVICIMVIFSGTVAHKSSFGQDRLILRLQIDIVDQKNYVNDLPELPPAPEDV 60
 QY 68 ETNCEWSAFSCFOKAQLKSAANTGNRRINVSIKLKKRPSTNAGRRQKRLTSPSCDS 127
 DB 61 KRHCERSAFSCFOKQLKAANTGNDEKLIINVLTKRKLPPTNAGRRQKRLTSPSCDS 120
 QY 128 YEKRPKEFLERFKSLQKMIHQHLS 153
 DB 121 YEKRPKEFLERFKSLQKMIHQHLS 146
 Db
 RESULT 5
 IL21_MOUSE STANDARD; PRT; 146 AA.
 ID IL21_MOUSE
 AC Q9BSI7;
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 24.
 DE Interleukin-21 precursor (IL-21).
 GN Name=IL21;
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX NCI
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP STRAIN=BALB/c;
 RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;
 RA Parrieh-Novak J., Dillon S.R., Nelson A., Sprecher C.,
 RA Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader C.,
 RA Burkhead S., Heipel M., Brandt C., Kujper J.L., Kramer J.,

RA Conklin D., Prensell S.R., Berry J., Shiota F., Bort S., Hamblly K.,
RA Madri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,
RA Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
RA Maurer W., Kaushansky K., Holly R.D., Foster D.;
RT "Interleukin 21 and its receptor are involved in NK cell expansion and
RT regulation of lymphocyte function.";
RL Nature 408:57-63(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE (mRNA).
RC STRAIN=BALB/c;
RA Gubbing C., Jun D., Junsong C., Fenshu Z.;
RT "Mouse Interleukin 21 can improve the anti-tumor effect of LAK
RT cells.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION AND SUBCELLULAR LOCATION.
RX PubMed=11970879; DOI=10.1016/S1074-7613(02)00295-9;
RA Kasalan M.T., Whitters M.J., Carter L.L., Lowe L.D., Juseif J.M.,
RA Deng B., Johnson K.A., Mitek J.S., Senices M., Konz R.F.,
RA Wurster A.L., Donaldson D.D., Collins M., Young D.A., Grusby M.J.;
RT "IL-21 limits NK cell responses and promotes antigen-specific T cell
RT activation: a mediator of the transition from innate to adaptive
RT immunity.";
RL Immunity 16:559-569(2002).
RN [4]
RP FUNCTION.
RX PubMed=12893770; DOI=10.1182/blood-2003-03-0669;
RA Brandt K., Bulfone-Paus S., Foster D.C., Rueckert R.;
RT "Interleukin-21 inhibits dendritic cell activation and maturation.";
RL Blood 102:4090-4098(2003).
RN [5]
RP FUNCTION.
RX PubMed=15100251;
RA Pene U., Gauchat J.F., Lecart S., Drouet E., Guglielmi P., Boulay V.,
RA Delwail A., Foster D., Lecron J.C., Yssel H.;
RT "IL-21 is a switch factor for the production of IgG1 and IgG3 by human
RT B cells.";
RL J. Immunol. 172:5154-5157(2004).
CC -I- FUNCTION. Cytokine with immunoregulatory activity. May promote the
CC transition between innate and adaptive immunity. Induces the
CC production of IgG(1) and IgG(3) in B-cells. May play a role in
CC proliferation and maturation of natural killer (NK) cells in
CC synergy with IL15. May regulate proliferation of mature B- and T-
CC cells in response to activating stimuli. In synergy with IL15 and
CC IL18 stimulates interferon gamma production in T-cells and NK
CC cells (By similarity). During T-cell mediated immune response may
CC inhibit dendritic cells (DC) activation and maturation.
CC -I- SUBCELLULAR LOCATION: Secreted protein.
CC -I- SIMILARITY: Belongs to the IL-21 family.
CC -----
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CC -----
DR EMBL: AF254070; AAC29349.1; -; mRNA.
DR EMBL: AY428162; AAR06254.1; -; mRNA.
DR Ensemble: ENSMUSG0000027718; Mus musculus.
DR MGI: MGI:1890474; Il21.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); IDA.
DR GO: GO:0045579; P:positive regulation of B cell differentiation; NAS.
DR GO: GO:0001783; P:programmed cell death, B cells; NAS.
KM Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 146 Interleukin-21.
FT FT Interleukin-21.
FT CARBOHYD 85 85 /FTid=PRO_0000015506.
FT DISULFID 64 115 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 71 118 Potential.
SQ SEQUENCE 146 AA; 16811 MW; D2527ED95BA15194 CRC64;

Query Match 57.2%; Score 486; DB 1; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-35;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERVICIAMVIFLGTIVHKSSSGQDRHIMRQLIDIVQKLVYNDLVEEFLPAPEDV 67
DB 1 MERTVLVAVIFLGTIVHKSSSGQDRHIMRQLIDIVQKLVYNDLVEEFLPAPEDV 60
QY 68 ETNCWMSAFSCFOKAQLKSNANTGNNERIIIVSIIKLKRKPPSTNAGRORRLTSPSCDS 127
DB 61 KGHCEHAAPAFQKAKLKPSNPGNNKTFILDLVAQLRRRLPARRGKKQGHIAKCPSCDS 120
QY 128 YEKKPKPEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPEFLERLKLQKMIHQHLS 146

RESULT 6
OSUSE2_MOUSE PRELIMINARY; PRT; 146 AA.
ID OSUSE2_MOUSE
AC OSUSE2;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 3.
DE Interleukin 21.
GN Name=Il21; ORFNames=DN-452A22.7-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pandian R.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: AL645982; CA126234.1; -; Genomic DNA.
DR Ensemble: ENSMUSG0000027718; Mus musculus.
SQ SEQUENCE 146 AA; 16811 MW; D2527ED95BA15194 CRC64;

Query Match 57.2%; Score 486; DB 2; Length 146;
Best Local Similarity 63.0%; Pred. No. 2.5e-35;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERVICIAMVIFLGTIVHKSSSGQDRHIMRQLIDIVQKLVYNDLVEEFLPAPEDV 67
DB 1 MERTVLVAVIFLGTIVHKSSSGQDRHIMRQLIDIVQKLVYNDLVEEFLPAPEDV 60
QY 68 ETNCWMSAFSCFOKAQLKSNANTGNNERIIIVSIIKLKRKPPSTNAGRORRLTSPSCDS 127
DB 61 KGHCEHAAPAFQKAKLKPSNPGNNKTFILDLVAQLRRRLPARRGKKQGHIAKCPSCDS 120
QY 128 YEKKPKPEFLERFKSLQKMIHQHLS 153
DB 121 YEKRTPEFLERLKLQKMIHQHLS 146

RESULT 7
IL21_PERMA STANDARD; PRT; 123 AA.
ID IL21_PERMA
AC O80XG2;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Interleukin-21 precursor (IL-21) (Fragment).
GN Name=Il21;
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Neotominae; Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP NUCLEOTIDE SEQUENCE (mRNA).

RA Schountz T., Buntiger A., Davenport B., Hegg T.:
 RT "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4
 RT CDNA's."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the
 CC transition between innate and adaptive immunity. Induces the
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in
 CC proliferation and maturation of natural killer (NK) cells in
 CC synergy with IL15. May regulate proliferation of mature B- and T-
 CC cells in response to activating stimuli. In synergy with IL15 and
 CC IL18 stimulates interferon gamma production in T-cells and NK
 CC cells (By similarity). During T-cell mediated immune response may
 CC inhibit dendritic cells (DC) activation and maturation (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-21 family.
 CC -----
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 CC -----
 DR EMBL: AY247761; AAD04420.1; -; mRNA.
 KM Cyokine; Glycoprotein; Signal.
 FT SIGNAL <1 10 Potential.
 FT CHAIN 11 123 Interleukin-21.
 FT CARBOHYD 77 77 N-linked (GlcNAc...) (Potential).
 FT DISULFID 56 107 Potential.
 FT DISULFID 63 110 Potential.
 FT NON_TER 1 1
 FT NON_TER 123 123
 SQ SEQUENCE 123 AA; 13945 MW; 8656C8EA95447E34 CRC64;
 Query Match 46.1%; Score 392; DB 1; Length 123;
 Best Local Similarity 60.2%; Pred. No. 5.1e-27;
 Matches 74; Conservative 24; Mismatches 25; Indels 0; Gaps 0;
 QY 16 MVIPLGLVHKSSQGDHMRMRLIDIVDQKNTVNDLVPEFLPAPEDEVFNCEWSA 75
 DB 1 VVIFLGTVAHKTSQRPDRPLRLRLHVLVDNVEQLKIVYNDLPDLPLPAPOVKESHCHSA 60
 QY 76 FSCFQKQLKSANTGNRRINIVSIIKKLRKPSPTNGRKHKLTPSCSCSYKKPKPE 135
 DB 61 PACQKAKLKPANSGSKTIIISDLVTQRLRLPLTKAEKKQSLVKCPSCSYKKPKPE 120
 QY 136 FLE 138
 DB 121 FLE 123
 RESULT 8
 Q58IU6 CHICK PRELIMINARY; PRT; 145 AA.
 ID Q58IU6 CHICK
 AC Q58IU6
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Interleukin 21.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Shao J., Dong W., Xiang L.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: AY943833; AAX40651.1; -; mRNA.
 SQ SEQUENCE 145 AA; 16637 MW; E70AB6A568CDA8E6 CRC64;

Query Match 20.2%; Score 171.5; DB 2; Length 145;
 Best Local Similarity 31.1%; Pred. No. 2.9e-07;
 Matches 47; Conservative 27; Mismatches 62; Indels 15; Gaps 5;
 QY 8 MERIVICLWVIFGLTVHKSSQGDHMRMRLIDIVDQKNTVNDLVPEFLPAPEDEV 67
 DB 1 MEMRIICMLFPCSWVLTRTSP----KAMKYQLSTIDHLKQVADKQVELHTPENP 56
 QY 68 ETNCEWSAFSCFQKQAKLSANTGNRRINIVSIIKKLRKPP--PSTNAGRQKRLTC-PS 124
 DB 57 GDGCLTLAVVCFQFGIHLKLOPKNSQVWATFAKTVKILRRFPLPV-----EEH---CESS 108
 QY 125 CDSYEKKPKPEFLERFKSLLOKIMHQLSSR 155
 DB 109 CESTYERKKPEFLNFSFKLMQKLFKSTAEK 139
 RESULT 9
 Q38I21 TETNG PRELIMINARY; PRT; 145 AA.
 ID Q38I21 TETNG
 AC Q38I21
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 22-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Interleukin 21.
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OC NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Head kidney;
 RA Wang H., Shao J., Xiang L., Dong W.;
 RT "Molecular cloning and expression analysis of an IL-21 homolog from
 RL Tetraodon nigroviridis."
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: DQ227693; ABB05043.1; -; mRNA.
 SQ SEQUENCE 145 AA; 16523 MW; F8BE28D1E3717818 CRC64;
 Query Match 14.1%; Score 119.5; DB 2; Length 145;
 Best Local Similarity 25.3%; Pred. No. 0.013;
 Matches 41; Conservative 29; Mismatches 57; Indels 35; Gaps 6;
 QY 8 MERIVICLWVIFGLTVHKSSQGDHMRMRLIDIVDQKNTVNDLVPEFLPAPEDEV 66
 DB 1 MKQVFLFLFAVCCMWMLADASSACSEKLEVRERLEGVNTLQN--RELL--LTTPKN 56
 QY 67 VERNCEWSAFSCF-----QKQKLSANTGNRRINIVSIIKKLRKPPPTNA 112
 DB 57 IREGCCSLARCFRDSIQENIKSTVRLQRLVYSLNNSHPAACINFC-----HSENA 108
 QY 113 GRQKRLTGPCSDSYKKPKPEFLERFKSLLOKIMHQLSSR 154
 DB 109 -----TQTCNSHPQEKVGFPSRLDSFIQAKSKLRSS 142
 RESULT 10
 IL15 FELCA STANDARD; PRT; 162 AA.
 ID IL15 FELCA
 AC Q97687
 DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1999, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Interleukin-15 precursor (IL-15).
 GN Name=IL15;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Flesipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE (MENA).
RC TISSUE=Lymph node;
RA Berger A.B., Dean G.A., Lavoy A.S.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytokine that stimulates the proliferation of T-
CC lymphocytes. Stimulation by IL-15 requires interaction of IL-15
CC with components of IL-2R, including IL-2R beta and probably IL-2R
CC gamma but not IL-2R alpha (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- SIMILARITY: Belongs to the IL-15 family.
CC -----
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CC -----
DR EMBL: AF108148; AAD05268.1; -; mRNA.
DR InterPro: IPR003443; Interleukin_15.
DR PANTHER: PTHR11323; Interleukin_15; 1.
DR Pfam: PF02372; IL15; 1.
DR Cytokine; Glycoprotein; Signal.
KW SIGNAL
FT PROPEP 1 29 Potential.
FT CHAIN 30 48 /FTid=PRO_0000015395.
FT FT 49 162 Interleukin_15.
FT CARBOHYD 104 104 /FTid=PRO_0000015396.
FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
FT DISULFID 83 133 N-linked (GlcNAc...) (Potential).
FT DISULFID 90 136 Potential.
SQ SEQUENCE 162 AA; 18412 MW; D8C7CEFF740110DD CRC64;

Query Match 12.5%; Score 106.5; DB 1; Length 162;
Best Local Similarity 26.0%; Pred. No. 0.21;
Matches 38; Conservative 25; Mismatches 58; Indels 25; Gaps 6;

QY 14 CWMYIFGLT---VHKSSGQGDHMTMRRLIDIVDQKNYVNDVPEFLPAPEDVETN 70
DB 30 CIPVFLISCTINAGLPKTEANQD--VISDLKTIKTIQSLHIDATLYTE---SDVHPN 82
QY 71 CEMSAFSCF---QKAOLKSANTGNERRIIVISIKLKRKPPSTNAGRGKRLT---CP 123
DB 83 CKVTAMKCFLELHVLSIESGNETITHQVEVITII-----LANSGLSKRNITTEGCK 134
QY 124 SCDSYEKKPKPEFLERFKSLIQKMIH 149
DB 135 ECCELKEKNIKEFLQSFVHIVQMFIN 160

RESULT 11
Q6FGX7 HUMAN PRELIMINARY; PRT; 135 AA.
AC Q6FGX7;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE IL15 protein (Interleukin 15, isoform 2).
GN Name=IL15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Halleck A., Ebert L., Moundinya M., Schick M., Bisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Hense S., Mar W.,
RA Korn B., Zhu D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

```

```

RC TISSUE=PCR/rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange S.J.,
RA Bata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalek U., Smallue D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Li C.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC100962; AA100963.1; -; mRNA.
DR EMBL: CR542007; CA646804.1; -; mRNA.
DR EMBL: AY720442; AAU21241.1; -; mRNA.
DR EMBL: CR541980; CA646777.1; -; mRNA.
DR EMBL: BC100961; AA100962.1; -; mRNA.
DR Ensembl: ENSG00000164136; Homo sapiens.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005126; F:hematopoietic/interferon-class (D200-domain...); IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR003443; Interleukin_15.
DR PANTHER: PTHR11323; Interleukin_15; 1.
DR Pfam: PF02372; IL15; 1.
SQ SEQUENCE 135 AA; 14912 MW; EB44F422096B143E CRC64;

Query Match 11.7%; Score 99.5; DB 2; Length 135;
Best Local Similarity 25.9%; Pred. No. 0.72;
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

QY 43 IDIVDQKNYVNDVPEF---LPAPEDVETNCMSAFSCF---QKAOLKSANTGNNE 93
DB 24 VIVISDLKK-IEDLIQSMHIDATLYTESDVHPSCVTAMKCFLELQVLSGSDA1HD 82
QY 94 RIIVNSIKLKRKPPSTNAGRGKRLTSCDSYEKKPKPEFLERFKSLIQKMIH 149
DB 83 TVENLII--LANSLSGNGVTES--GCKECELKEKNIKEFLQSFVHIVQMFIN 133

RESULT 12
IL15 HUMAN STANDARD; PRT; 162 AA.
ID IL15 HUMAN
AC P40933; O00440; O43512; Q93058; Q9UBA3;
DT 01-FEB-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1995, sequence version 1.
DT 07-FEB-2006, entry version 43.
DE Interleukin-15 precursor (IL-15).
GN Name=IL15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 CC Homo.
 CC NCBI_TaxID=9606;
 CC [1]
 CC NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA).
 CC TISSUE=Bone marrow;
 CC MEDLINE=94233380; PubMed=8178155;
 CC Grabsbein K.H., Biesenman J., Shanebeck K., Rauch C., Srinivasan S.,
 CC Fung V., Beers C., Richardson J., Schoenborn M.A., Andieh M.,
 CC Johnson L., Alderson M.R., Watson J.D., Anderson D.M., Giri J.G.;
 CC "Cloning of a T cell growth factor that interacts with the beta chain
 CC of the interleukin-2 receptor.";
 CC Science 264:965-968(1994).
 CC [2]
 CC NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA).
 CC Krause H., Jandrig B., Wernicke C., Bulfone-Paus S., Pohl T.,
 CC Diamantstein T.;
 CC Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.
 CC [3]
 CC NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA).
 CC TISSUE=Lung cancer;
 CC MEDLINE=96218668; PubMed=8668345;
 CC Meazza R., Verdiani S., Biassoni R., Coppolecchia M., Gaggero A.,
 CC Orongo A.M., Colombo M.P., Azzarone B., Ferrini S.;
 CC "Identification of a novel interleukin-15 (IL-15) transcript isoform
 CC generated by alternative splicing in human small cell lung cancer cell
 CC lines.";
 CC Oncogene 12:2187-2192(1996).
 CC [4]
 CC NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA).
 CC TISSUE=Testis;
 CC MEDLINE=98070771; PubMed=9405632; DOI=10.1073/pnas.94.26.14444;
 CC Tagaya Y., Kurys G., Thies T.A., Losi T.A., Azimi N., Hanover J.A.,
 CC Bamford R.N., Waldmann T.A.;
 CC "Generation of secretable and nonsecretable interleukin 15 isoforms
 CC through alternate usage of signal peptides.";
 CC Proc. Natl. Acad. Sci. U.S.A. 94:14444-14449(1997).
 CC [5]
 CC NUCLEOTIDE SEQUENCE (ISOFORM 3).
 CC Meazza R., Ferrini S.;
 CC "Expression of two IL-15 mRNA isoforms in human tumors does not
 CC correlate with secretion: role of different signal peptides.";
 CC Submitted (AAR-1997) to the EMBL/Genbank/DBJ databases.
 CC [6]
 CC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM IL15-S48AA).
 CC TISSUE=Colon;
 CC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 CC Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 CC Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
 CC Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 CC Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 CC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 CC Biskreby R.W., Touchman J.W., Green E.D., Dickson M.C.,
 CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 CC Butlerfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
 CC Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 CC "Generation and initial analysis of more than 15,000 full-length human
 CC and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC [7]
 CC NUCLEOTIDE SEQUENCE OF 49-162.
 CC TISSUE=Epidermis;
 CC Sorel M.A., Jacques Y.;
 CC "IL15 expression in human keratinocytes.";
 CC Submitted (OCT-1994) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: Cytokine that stimulates the proliferation of T-
 CC lymphocytes. Stimulation by IL-15 requires interaction of IL-15
 CC with components of IL-2R, including IL-2R beta and probably IL-2R
 CC gamma but not IL-2R alpha.
 CC -1- SUBCELLULAR LOCATION: Secreted (IL15-S48AA). IL15-S21AA is not
 CC secreted, but rather is stored intracellularly, appearing in the
 CC nucleus and cytoplasmic components.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=IL15-S48AA;
 CC IsoId=P40933-1; Sequence=Displayed;
 CC Name=IL15-S21AA;
 CC IsoId=P40933-2; Sequence=VSP_002660;
 CC Name=3;
 CC IsoId=P40933-3; Sequence=VSP_002661;
 CC -1- TISSUE SPECIFICITY: Most abundant in placenta and skeletal muscle.
 CC It is also detected in the heart, lung, liver and kidney. IL15-
 CC S21AA is preferentially expressed in tissues such as testis and
 CC thymus.
 CC -1- SIMILARITY: Belongs to the IL-15 family.
 CC -1- DATABASE: NAME=R&D Systems' cytokine source book: IL15;
 CC WWW="http://www.rndsystems.com/asp/9_statebuilder.asp?bodyId=209".
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
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 CC EMBL: U14407; AA21551.1; -; mRNA.
 CC EMBL: X91233; CA62616.1; -; Genomic_DNA.
 CC EMBL: X94223; CA63914.1; -; mRNA.
 CC EMBL: X94222; CA63913.1; -; mRNA.
 CC EMBL: AF031167; AA897518.1; -; mRNA.
 CC EMBL: Y09908; CA71044.1; -; mRNA.
 CC EMBL: BC018149; AA18149.1; -; mRNA.
 CC EMBL: Z38000; CA86100.1; -; mRNA.
 CC Ensembl: ENSG00000164136; Homo sapiens.
 CC HGNC: HGNC:5977; IL15.
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 CC GO: GO:0004871; F:signal transducer activity; TAS.
 CC GO: GO:0007267; P:cell-cell signaling; TAS.
 CC GO: GO:0006955; P:immune response; TAS.
 CC GO: GO:0008284; P:positive regulation of cell proliferation; TAS.
 CC GO: GO:0007165; P:signal transduction; TAS.
 CC InterPro: IPR003443; Interleukin_15.
 CC PANTHER: PTHR11323; Interleukin_15; 1.
 CC Pfam: PF02372; IL15; 1.
 CC KX Alternative splicing; Cytokine; Glycoprotein; Signal.
 CC SIGNAL 1 29 Potential.
 CC PROPEP 30 48 Potential.
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 CC FT Interleukin-15.
 CC FT /FTid=PRO_0000015394.
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 CC FT DISULFID 83 133 Potential.
 CC FT DIPEPTID 90 136 Potential.
 CC FT VAAPSPIC 1 47 MRISPHLRGSIQCYCLILNSHFLTEAGHVFLLGCFSA
 CC FT GLPKTE -> MDPVOQIFSPFLIASVYMSR (in
 CC isoform 3).
 CC FT VAAPSPIC 1 37 /FTid=VSP_002661.
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 CC FT MVLGTIDCS (in isoform IL15-S21AA).
 CC FT /FTid=VSP_002660.
 CC FT E -> K (in Ref. 4).
 CC FT CONFLICT 141 141 E -> K (in Ref. 4).
 CC FT SEQUENCE 162 AA; 18086 MW; 0CE0520C1D837952 CRC64;
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 CC Query Match 11.7%; Score 99.5; DB 1; Length 162;
 CC Best Local Similarity 25.9%; Pred. No. 0.88;
 CC Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

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Qy 43 IDIVDOLKONYVNDLVPF-----LPAPEDVETNCESAFSCF-----OKAOLKSANTGNNE 93
Db 51 VNIYSDUKK-IEDIQSMHIDATITYESDVHPSCKVTAMKCFLELLOVISLESQDASIH 109
Qy 94 RIINVSIKUKRKPSTNAGRGHRLTSPSCDSYEKKPPEFLERFKSLLOKMIH 149
Db 110 TVEHLIT--LANNLSNGNVTES---GCKECELLEKNIKEFLQSFVHIQWFMIN 160

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AC Q49528;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Interleukin 15, isoform 1.
GN Name=IL15;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
NCBI_TaxID=9606;
RN Nucleotide Sequence.
RP Tissue=PCR rescued clones;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Mausina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uebin T.B., Toshimuki S., Garinoti P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Vallian D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RA "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN Nucleotide Sequence.
RP Tissue=PCR rescued clones;
RC NIH MGC Project;
RL Submitted (Aug-2005) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs license
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DR EMBL: BCJ00963; AA100964.1; mRNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005126; F:hematopoietic/interferon-class (D200-domain. . .); IEA.
DR GO: GO:0006955; P:immune response; IEA.
SQ SEQUENCE 162 AA; 18086 MW; 0CE0520C1D8379E2 CRC64;

Query Match 11.7%; Score 99.5; DB 2; Length 162;
Best Local Similarity 23.9%; Pred. No. 0.88; Indels 15; Gaps 5;
Matches 30; Conservative 23; Mismatches 48;

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AC Q59902;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Interleukin-21.
GN Name=IL-21;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
NCBI_TaxID=31033;
RN Nucleotide Sequence.
RP PubMed=15592926; DOI=10.1007/s00251-004-0741-7;
RA Bird S., Zou J., Kono T., Sakai M., Martins Dijkstra J., Secombe C.;
RT "Characterisation and expression analysis of interleukin 2 (IL-2) and
RT IL-21 homologues in the Japanese pufferfish, Fugu rubripes, following
RT the discovery by synteny."
RL Immunogenetics 56:909-923(2005).
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DR EMBL: AJ844554; CAH59638.1; mRNA.
DR EMBL: AJ84837; CAE50922.2; Genomic DNA.
SQ SEQUENCE 155 AA; 17777 MW; 61DEFE96BD52945E CRC64;

Query Match 11.6%; Score 98.5; DB 2; Length 155;
Best Local Similarity 23.6%; Pred. No. 1;
Matches 37; Conservative 33; Mismatches 64; Indels 23; Gaps 6;

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Db 60 ENIGDCCLSLALCKFR-----NFKEIFSLTDPQKLYRSLNLTLEKGLDFCDS 110
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DT 27-SEP-2005, sequence version 1.
DT 07-MAR-2006, entry version 6.
DE Interleukin-15 precursor (IL-15).
GN Name=IL15;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
NCBI_TaxID=9986;
RN Nucleotide Sequence [RNA], AND TISSUE SPECIFICITY.
RP PubMed=1597671; DOI=10.1016/j.yetimm.2005.04.013;
RA Xiong C., Hixson P.M., Mendoza L.H., Smith C.W.;
RT "Cloning and expression of rabbit interleukin-15."
RL Vet. Immunol. Immunopathol. 107:131-141(2005).
CC -1- FUNCTION: Cytokine that stimulates the proliferation of T-
CC lymphocytes. Stimulation by IL-15 requires interaction of IL-15
CC with components of IL-2R, including IL-2R beta and probably IL-2R

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CC      gamma but not IL-2R alpha (By similarity).
CC      -1- SUBCELLULAR LOCATION: Secreted protein.
CC      -1- TISSUE SPECIFICITY: Expressed in many tissues including heart,
CC      spleen, lung, liver, muscle and kidney (at mRNA level). Expressed
CC      in many tissues including heart, spleen, lung, liver, muscle and
CC      kidney (at protein level).
CC      -1- SIMILARITY: Belongs to the IL-15 family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL: DO157452; AA282803.1; -. mRNA.
DR      InterPro: IPR003443; Interleukin_15.
DR      PANTHER: PTHR11323; Interleukin_15; 1.
DR      Pfam: PF02372; IL15; 1.
DR      Cytokine; Glycoprotein; Signal.
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 Job time : 91.3314 secs

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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:51:46; Search time 16.2 Seconds
(without alignments)
875.306 Million cell updates/sec

Title: US-10-659-684-2
Perfect score: 850
Sequence: 1 MRSSPGNNRIVICLMTVFL.....LLQKMIHQHLSRTHGSDDS 162

Scoring table:
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Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pap:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pap:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PTUS_COMB.pap:*
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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfilest.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	850	100.0	162	2	US-09-522-217-2 Sequence 2, Appli
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3	850	100.0	162	2	US-10-295-723-2 Sequence 2, Appli
4	850	100.0	162	2	US-09-825-561A-10 Sequence 10, Appli
5	850	100.0	162	2	US-10-282-622-2 Sequence 2, Appli
6	850	100.0	174	2	US-09-949-016-10307 Sequence 10307, A
7	831	97.8	162	2	US-10-282-622-6 Sequence 4, Appli
8	758	89.2	147	2	US-10-282-622-4 Sequence 4, Appli
9	695.5	81.8	519	2	US-09-522-217-85 Sequence 85, Appli
10	695.5	81.8	519	2	US-09-923-246-85 Sequence 85, Appli
11	695.5	81.8	519	2	US-10-295-723-85 Sequence 85, Appli
12	486	57.2	146	2	US-09-522-217-56 Sequence 56, Appli
13	486	57.2	146	2	US-09-923-246-56 Sequence 56, Appli
14	486	57.2	146	2	US-10-295-723-56 Sequence 56, Appli
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42	99.5	11.7	162	1	US-08-725-969-2 Sequence 2, Appli
43	99.5	11.7	162	1	US-08-794-524-2 Sequence 2, Appli
44	99.5	11.7	162	2	US-08-842-947-6 Sequence 6, Appli
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ALIGNMENTS

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RESULT 1
US-09-522-217-2
; Sequence 2, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Grose, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-522-217-2
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Best Local Similarity 100.0%; Pred. No. 1.4e-86;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	LPAPEDVTNEMSAFSCFOAKOLKSANTGNNRIINVSICKLARKKPPSTNAGRORGRRL	120
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DB	121	TCPSGDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSDDS	162

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; Sequence 2, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
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; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2

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Best Local Similarity 100.0%; Pred. No. 1,4e-86;
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RESULT 3
US-10-295-723-2
; Sequence 2, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
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; PRIOR FILING DATE: 1999-03-11
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; PRIOR FILING DATE: 1999-07-01
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-2

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Best Local Similarity 100.0%; Pred. No. 1,4e-86;
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DB      61 LPAPEDVETNCESAFSCFQKQKLSANTGNNERIINVSIKLKRKPPSTNAGRQGRRL 120

QY      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
      |||||||
DB      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 4
US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match      100.0%; Score 850; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,4e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MRSSPGNMERIVICLWYIFLGTLVHKSSSGODRHMIRMQLDIDVDQLKNYVNDLVPEF 60
      |||||||
DB      1 MRSSPGNMERIVICLWYIFLGTLVHKSSSGODRHMIRMQLDIDVDQLKNYVNDLVPEF 60

QY      61 LPAPEDVETNCESAFSCFQKQKLSANTGNNERIINVSIKLKRKPPSTNAGRQGRRL 120
      |||||||
DB      61 LPAPEDVETNCESAFSCFQKQKLSANTGNNERIINVSIKLKRKPPSTNAGRQGRRL 120

QY      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
      |||||||
DB      121 TCPSCDSEYEKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
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RESULT 5
US-10-282-622-2
Sequence 2, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-282-622-2

Query Match 100.0%; Score 850; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.4e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRSSPGNNRIVICLVIFLGLTVHKSSSGODRHMIMROLIDIVDOLKNYVNDLVEEF 60
Db 1 MRSSPGNNRIVICLVIFLGLTVHKSSSGODRHMIMROLIDIVDOLKNYVNDLVEEF 60
Oy 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIIVSIKLRKRPSTNAGRORQKRL 120
Db 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIIVSIKLRKRPSTNAGRORQKRL 120
Oy 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 6
US-09-949-016-10307
Sequence 10307, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10307
LENGTH: 174
TYPE: PRT
ORGANISM: Human
US-09-949-016-10307

Query Match 100.0%; Score 850; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 1.5e-86;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MRSSPGNNRIVICLVIFLGLTVHKSSSGODRHMIMROLIDIVDOLKNYVNDLVEEF 60
Db 13 MRSSPGNNRIVICLVIFLGLTVHKSSSGODRHMIMROLIDIVDOLKNYVNDLVEEF 72

Oy 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIIVSIKLRKRPSTNAGRORQKRL 120
Db 73 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIIVSIKLRKRPSTNAGRORQKRL 132
Oy 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db 133 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 174

RESULT 7
US-10-282-622-6
Sequence 6, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 162
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zalpahl1 ligand Q153D/I156D
US-10-282-622-6

Query Match 97.8%; Score 831; DB 2; Length 162;
Best Local Similarity 98.1%; Pred. No. 1.8e-84;
Matches 159; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MRSSPGNNRIVICLVIFLGLTVHKSSSGODRHMIMROLIDIVDOLKNYVNDLVEEF 60
Db 1 MRSSPGNNRIVICLVIFLGLTVHKSSSGODRHMIMROLIDIVDOLKNYVNDLVEEF 60
Oy 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIIVSIKLRKRPSTNAGRORQKRL 120
Db 61 LPAPEDVTNCWMSAFSCFOQAOLKSANTGNNRINIIVSIKLRKRPSTNAGRORQKRL 120
Oy 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db 121 TCPSCDSYEKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 8
US-10-282-622-4
Sequence 4, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932ak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 147
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zalpahl1 ligand Q153ST/I156D
US-10-282-622-4

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Query Match      89.2%; Score 758; DB 2; Length 147;
Best Local Similarity 98.6%; Pred. No. 2.1e-76;
Matches 145; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MRSSPGNMRIVICLWVIFLGLTVHKSSQGDHRMIRMQIDIVDQKNYVNDLVPEF 60
Db 1 MDSSFGNMRIVICLWVIFLGLTVHKSSQGDHRMIRMQIDIVDQKNYVNDLVPEF 60

Qy 61 LPAPDEVETNCWMSAFSCFQAOLKSANTGNMERIINVSIKLKRKPPSTNAGRQKRL 120
Db 61 LPAPDEVETNCWMSAFSCFQAOLKSANTGNMERIINVSIKLKRKPPSTNAGRQKRL 120

Qy 121 TCPSCDSEYKKPKPEFLERFKSLQKM 147
Db 121 TCPSCDSEYKKPKPEFLERFKSLQKM 147

RESULT 9
US-09-522-217-85
; Sequence 85, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide
US-09-522-217-85

Query Match      81.8%; Score 695.5; DB 2; Length 519;
Best Local Similarity 95.7%; Pred. No. 9.6e-69;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 23 LVHSSSGODRHMIRMQIDIVDQKNYVNDLVPEFLPAPDEVETNCWMSAFSCFOKA 82
Db 383 LVPRGS---QDRHMIRMQIDIVDQKNYVNDLVPEFLPAPDEVETNCWMSAFSCFOKA 439

Qy 83 QLSKANTGNMERIINVSIKLKRKPPSTNAGRQKRLTPSCDSYEKKPKPEFLERFKS 142
Db 440 QLSKANTGNMERIINVSIKLKRKPPSTNAGRQKRLTPSCDSYEKKPKPEFLERFKS 499

Qy 143 LQKMIHQHLSRTHGSEDS 162
Db 500 LQKMIHQHLSRTHGSEDS 519

RESULT 10
US-09-923-246-85
; Sequence 85, Application US/09923246
```

```
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; EARLIER FILING DATE: 2001-08-03
; EARLIER APPLICATION NUMBER: US/09/522,217
; EARLIER FILING DATE: EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polypeptide
US-09-923-246-85

Query Match      81.8%; Score 695.5; DB 2; Length 519;
Best Local Similarity 95.7%; Pred. No. 9.6e-69;
Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

Qy 23 LVHSSSGODRHMIRMQIDIVDQKNYVNDLVPEFLPAPDEVETNCWMSAFSCFOKA 82
Db 383 LVPRGS---QDRHMIRMQIDIVDQKNYVNDLVPEFLPAPDEVETNCWMSAFSCFOKA 439

Qy 83 QLSKANTGNMERIINVSIKLKRKPPSTNAGRQKRLTPSCDSYEKKPKPEFLERFKS 142
Db 440 QLSKANTGNMERIINVSIKLKRKPPSTNAGRQKRLTPSCDSYEKKPKPEFLERFKS 499

Qy 143 LQKMIHQHLSRTHGSEDS 162
Db 500 LQKMIHQHLSRTHGSEDS 519

RESULT 11
US-10-295-723-85
; Sequence 85, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; EARLIER FILING DATE: 2002-11-15
; EARLIER APPLICATION NUMBER: 09/522,217
; EARLIER FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
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PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 60/142,013
 PRIOR FILING DATE: 1999-07-01
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 85
 LENGTH: 519
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: MBP-human zalpha11 Ligand fusion polypeptide
 US-10-295-723-85

Query Match 81.8%; Score 695.5; DB 2; Length 519;
 Best Local Similarity 95.7%; Pred. No. 9,66-69;
 Matches 134; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 23 LVHSSQSGDRHMRKQLIDIVDLKQYVNDLVPEFLPAPEVETNCESAFSCFOKA 82
 DB 383 LVPEGS--QDRHMRKQLIDIVDLKQYVNDLVPEFLPAPEVETNCESAFSCFOKA 439
 QY 83 QLSANTGNNRIRIIVSIKLLKRPSTNAGRQKRLTCSYSEKPKPEFLERFKS 142
 DB 440 QLSANTGNNRIRIIVSIKLLKRPSTNAGRQKRLTCSYSEKPKPEFLERFKS 499
 QY 143 LLOKMIHQHLSRTHGSEDS 162
 DB 500 LLOKMIHQHLSRTHGSEDS 519

RESULT 12
 US-09-522-217-56
 Sequence 56, Application US/09522217
 Patent No. 6307024
 GENERAL INFORMATION:
 APPLICANT: No. 6307024ak, Julia E.
 APPLICANT: Premeil, Scott R.
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Foster, Donald C.
 APPLICANT: Holly, Richard D.
 APPLICANT: Gross, Jane A.
 APPLICANT: Johnston, Janet V.
 APPLICANT: Nelson, Andrew J.
 APPLICANT: Dillon, Stacey R.
 APPLICANT: Hammond, Angela K.
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
 FILE REFERENCE: 99-16
 CURRENT APPLICATION NUMBER: US/09/522,217
 EARLIER FILING DATE: 2000-03-09
 EARLIER APPLICATION NUMBER: US 60/123,547
 EARLIER FILING DATE: 1999-03-09
 EARLIER APPLICATION NUMBER: US 60/123,904
 EARLIER FILING DATE: 1999-03-11
 EARLIER APPLICATION NUMBER: US 60/142,013
 EARLIER FILING DATE: 1999-07-01
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 56
 LENGTH: 146
 TYPE: PRT
 ORGANISM: mus musculus
 US-09-522-217-56

Query Match 57.2%; Score 486; DB 2; Length 146;
 Best Local Similarity 63.0%; Pred. No. 3,7e-46;
 Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
 QY 8 MERIVICLWVIFGLTVHSSQSGDRHMRKQLIDIVDLKQYVNDLVPEFLPAPEV 67
 DB 1 MERTLVCLVVFIFGLTVHSSQSGDRHMRKQLIDIVDLKQYVNDLVPEFLPAPEV 60
 QY 68 ETNCESAFSCFOKAQLKSANTGNNRIRIIVSIKLLKRPSTNAGRQKRLTCSYSE 127

DB 61 KGHCEHAFAFCFOKAKLKPSNPNNKTFIIDLVAQLRRRLPARRGGKQKHIAKCPSCDS 120
 QY 128 YEKKPKPEFLERFKSLLOKMIHQHLS 153
 DB 121 YEKRTPEFLERLKLWLOKMIHQHLS 146

RESULT 13
 US-09-923-246-56
 Sequence 56, Application US/09923246
 Patent No. 6605272
 GENERAL INFORMATION:
 APPLICANT: No. 6605272ak, Julia E.
 APPLICANT: Premeil, Scott R.
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Foster, Donald C.
 APPLICANT: Holly, Richard D.
 APPLICANT: Gross, Jane A.
 APPLICANT: Johnston, Janet V.
 APPLICANT: Nelson, Andrew J.
 APPLICANT: Dillon, Stacey R.
 APPLICANT: Hammond, Angela K.
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
 FILE REFERENCE: 99-16
 CURRENT APPLICATION NUMBER: US/09/923,246
 EARLIER FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
 PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 56
 LENGTH: 146
 TYPE: PRT
 ORGANISM: mus musculus
 US-09-923-246-56

Query Match 57.2%; Score 486; DB 2; Length 146;
 Best Local Similarity 63.0%; Pred. No. 3,7e-46;
 Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;
 QY 8 MERIVICLWVIFGLTVHSSQSGDRHMRKQLIDIVDLKQYVNDLVPEFLPAPEV 67
 DB 1 MERTLVCLVVFIFGLTVHSSQSGDRHMRKQLIDIVDLKQYVNDLVPEFLPAPEV 60
 QY 68 ETNCESAFSCFOKAQLKSANTGNNRIRIIVSIKLLKRPSTNAGRQKRLTCSYSE 127
 DB 61 KGHCEHAFAFCFOKAKLKPSNPNNKTFIIDLVAQLRRRLPARRGGKQKHIAKCPSCDS 120
 QY 128 YEKKPKPEFLERFKSLLOKMIHQHLS 153
 DB 121 YEKRTPEFLERLKLWLOKMIHQHLS 146

RESULT 14
 US-10-295-723-56
 Sequence 56, Application US/10295723
 Patent No. 6686178
 GENERAL INFORMATION:
 APPLICANT: No. 6686178ak, Julia E.
 APPLICANT: Premeil, Scott R.
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Foster, Donald C.
 APPLICANT: Holly, Richard D.
 APPLICANT: Gross, Jane A.
 APPLICANT: Johnston, Janet V.
 APPLICANT: Nelson, Andrew J.
 APPLICANT: Dillon, Stacey R.
 APPLICANT: Hammond, Angela K.
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:52:41 ; Search time 58.7829 Seconds
(without alignments)
1276.576 Million cell updates/sec

Title: US-10-659-684-2

Perfect score: 850

Sequence: 1 MRSSPGNMERIVICLWVIFL.....LLQKMIHQHLSRTHGSEDS 162

Scoring table: BLOSUM62

Searched: Gap0 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 209797

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	850	100.0	162	3	US-09-923-246-2
2	850	100.0	162	3	US-09-825-561A-10
3	850	100.0	162	3	US-09-972-218A-19
4	850	100.0	162	4	US-10-264-634-19
5	850	100.0	162	4	US-10-295-723-2
6	850	100.0	162	4	US-10-283-622-2
7	850	100.0	162	4	US-10-456-780-2
8	850	100.0	162	4	US-10-659-684-2
9	850	100.0	162	4	US-10-620-169-2
10	850	100.0	162	5	US-10-872-087-10
11	850	100.0	162	5	US-10-787-442-2
12	850	100.0	162	5	US-10-951-239-2
13	850	100.0	162	5	US-10-775-204-2177
14	850	100.0	162	6	US-11-174-398-2
15	850	100.0	162	6	US-11-134-489-2
16	850	100.0	162	6	US-11-132-947-9
17	850	100.0	162	6	US-11-197-488-19
18	840	98.8	160	6	US-11-197-221-1
19	831	97.8	162	4	US-10-282-622-6
20	831	97.8	162	4	US-11-174-398-6
21	758	89.2	147	6	US-10-282-622-4
22	758	89.2	147	6	US-11-174-398-4
23	708.5	83.4	742	5	US-10-775-204-2167
24	706	83.1	133	5	US-10-867-992-19
25	695.5	81.8	519	3	US-09-923-246-85
26	695.5	81.8	519	4	US-10-295-723-85
27	695.5	81.8	519	4	US-10-659-684-85

28	695.5	81.8	519	5	US-10-787-442-85	Sequence 85, Appl
29	695	81.8	131	5	US-10-867-992-16	Sequence 16, Appl
30	695	81.8	131	6	US-11-132-947-2	Sequence 2, Appl
31	661	77.8	133	5	US-10-867-992-12	Sequence 12, Appl
32	656	77.2	133	5	US-10-867-992-14	Sequence 14, Appl
33	650	76.5	131	5	US-10-867-992-10	Sequence 10, Appl
34	648	76.2	152	6	US-11-132-947-12	Sequence 12, Appl
35	645	75.9	131	5	US-10-867-992-4	Sequence 4, Appl
36	645	75.9	131	5	US-10-867-992-6	Sequence 6, Appl
37	644	75.8	131	5	US-10-867-992-8	Sequence 8, Appl
38	642	75.5	131	5	US-10-867-992-2	Sequence 2, Appl
39	486	57.2	146	3	US-09-923-246-56	Sequence 56, Appl
40	486	57.2	146	3	US-09-825-561A-47	Sequence 47, Appl
41	486	57.2	146	4	US-10-295-723-56	Sequence 56, Appl
42	486	57.2	146	4	US-10-456-780-4	Sequence 4, Appl
43	486	57.2	146	4	US-10-659-684-56	Sequence 56, Appl
44	486	57.2	146	5	US-10-872-087-47	Sequence 47, Appl
45	486	57.2	146	5	US-10-787-442-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-923-246-2
Sequence 2, Application US/09923246
Patent No. US20020128446A1
GENERAL INFORMATION:
APPLICANT: No. US20020128446A1ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US/09/923,246
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-09-923-246-2

Query Match : 100.0%; Score 850; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRSSPGNMERIVICLWVIFLCTLVHKSSSQGDHMRMLIIVDLKRYVNDLVPEF	60
DB	1	MRSSPGNMERIVICLWVIFLCTLVHKSSSQGDHMRMLIIVDLKRYVNDLVPEF	60
QY	61	LPAPEDVTNCEWMAFSCFOAKOLKSANTGNNEIRIIVSIKLLRKXPSTNAGRORL	120
DB	61	LPAPEDVTNCEWMAFSCFOAKOLKSANTGNNEIRIIVSIKLLRKXPSTNAGRORL	120
QY	121	TCPSCDSEYKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS	162
DB	121	TCPSCDSEYKKPKPEFLERFKSLLOKMIHQHLSRTHGSEDS	162

```
RESULT 2
US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. US2002013767A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US2002013767A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match      100.0%; Score 850; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIDVQLKNYVNDLVPEF 60
Db      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIDVQLKNYVNDLVPEF 60

Qy      61 LPAPDEVETNCESAFSCFOKAOLKSANTGNERRIINVSICKLKRKPPSTNAGRQGRHL 120
Db      61 LPAPDEVETNCESAFSCFOKAOLKSANTGNERRIINVSICKLKRKPPSTNAGRQGRHL 120

Qy      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 3
US-09-972-218A-19
; Sequence 19, Application US/09972218A
; Publication No. US20030049798A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Laura
; APPLICANT: Whiteley, Matthew J
; APPLICANT: Collins, Mary
; APPLICANT: Young, Deborah A.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lowe, Leslie D.
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: NO-1, Member of the Cytokine Receptor Family
; FILE REFERENCE: 22058-552C1p2
; CURRENT APPLICATION NUMBER: US/09/972,218A
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/569384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/560766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US/6057128
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-09-972-218A-19

Query Match      100.0%; Score 850; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIDVQLKNYVNDLVPEF 60
Db      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIDVQLKNYVNDLVPEF 60

Qy      61 LPAPDEVETNCESAFSCFOKAOLKSANTGNERRIINVSICKLKRKPPSTNAGRQGRHL 120
Db      61 LPAPDEVETNCESAFSCFOKAOLKSANTGNERRIINVSICKLKRKPPSTNAGRQGRHL 120

Qy      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 4
US-10-264-634-19
; Sequence 19, Application US/10264634
; Publication No. US20030108549A1
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra et al.
; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor Ac
; FILE REFERENCE: G15320-P3
; CURRENT APPLICATION NUMBER: US/10/264,634
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 09/040,005
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 09/560,766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/569,384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/972,218
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/373,746
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Human
US-10-264-634-19

Query Match      100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIDVQLKNYVNDLVPEF 60
Db      1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHMIRMQLDIDVQLKNYVNDLVPEF 60

Qy      61 LPAPDEVETNCESAFSCFOKAOLKSANTGNERRIINVSICKLKRKPPSTNAGRQGRHL 120
Db      61 LPAPDEVETNCESAFSCFOKAOLKSANTGNERRIINVSICKLKRKPPSTNAGRQGRHL 120

Qy      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162
Db      121 TCPSGDSYEKKPPEFLERFKSLLOKMIHQHLSRTHGSEDS 162

RESULT 5
US-10-295-723-2
; Sequence 2, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
```



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APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
FILE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-723-2

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Query Match	100.0%	Score 850;	DB 4;	Length 162;
Best Local Similarity	100.0%	Pred. No. 2e-81;		
Matches 162; Conservative	0;	Mismatches	0;	Gaps 0

QY 1 MRSSPGNMERIVICLWVIFLGTLVHKSSSGODRHIMRQLIDI VPD LKNVYNDLVPEF 60

Dd 1 MRSSGNNRRIYICLAVIFLGLYHKSSQSGDDRMIMRQLDLDVDDQKRVNDLVPEE 60

Qy 61 LPAPEDVTNCEWSAFSCFQKQLKSANTGNRRILNISIKLKKRPPSTNAGRQKHRL 120

Dd 61 LPAPEDVTNCEWSAFSCFQKQLKSANTGNRRILNISIKLKKRPPSTNAGRQKHRL 120

Qy 121 TCPCSDSYEKKPKKEFLERFSLQKMTHQHLSRTHGSEDS 162
|||||
Db 121 TCPCSDSYEKKPKPEFLERFSLQKMTHQHLSRTHGSEDS 162
|||||

RESULT 6
US-10-282-622-2
; Sequence 2, Application US/10282622
; Publication No. US20030134390A1

```

1  GENERAL INFORMATION:
2  APPLICANT: Presnell, Scott R.
3  APPLICANT: West, James W.
4  APPLICANT: No. US20030134390A1ak, Julia E.
5  TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
6  FILE REFERENCE: 01-37
7  CURRENT APPLICATION NUMBER: US/10/282,622
8  CURRENT FILING DATE: 2002-10-28
9  PRIOR APPLICATION NUMBER: 60/337,586
10 PRIOR FILING DATE: 2001-11-05
11 NUMBER OF SEQ ID NOS: 30
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 2
14 LENGTH: 162

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ORGANISM: Homo sapiens
US-10-282-622-2

Query Match	100.0%;	Score 850;	DB 4;	Length 162;
Best Local Similarity	100.0%;	Pred. No. 2e-81;		
Matches 162;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

Qy 1 MRSSGNNMERIYICLMVIFELGTLVHKSSSQGDRIHRRQLDIDYDQKATVNDLVEPF 60

Db 1 MRSSGNNMERIYICLMVIFELGTLVHKSSSQGDRIHRRQLDIDYDQKATVNDLVEPF 60

Qy 61 LPAPDEVETNCESMAFSCFCQAKQLKSANTGNNERIINVSIKTLKKRPSTNAGRQKRL 120

Db 61 LPAPEDVETNCWMAFSCFQAQQLSANTGNNERINVSIKLKPKPSTNAGRQKARL 120

QY 121 TCPSCDSYEKKPPKEFLERFKSLLOQMTHQHLSTHTSDEDS 162

Db 121 TCPSCDSYEKKPPKEFLERFKSLLOQMTHQHLSTHTSDEDS 162

RESULT 7
US-10-456-780-2

;; Sequence 2, Application US/10456780
;; Publication No. US20040009150A1
: GENERAL INFORMATION:

: APPLICANT: Nelson, Andrew J.
 : APPLICANT: Hughes, Steven D.
 : APPLICANT: Holly, Richard D.
 : TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
 : TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
 : FILE REFERENCE: 03-08

```

; CURRENT APPLICATION NUMBER: US/10/456,780
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0

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```
; SEQ ID NO 2
; LENGTH: 162
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-456-780-2
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Query Match	100.0%	Score 850	DB 4	Length 162
Best Local Similarity	100.0%	Pred. No. 2e-81		
Matches 162; Conservative	0	Mismatches	0	Indels 0
				Gaps 0

1 MRSSPGNNRIVICLWIFLGTLVHKKSSOGDRHMRKOLIDVDQLKNVNDLVPF 60
QY

Db 1 MRSSGNNRIVICLVVIFLGLVHKSSSGQGDRIIMRQLIDIVDOLKNVYNDLVEEF 60

Qy 61 LPAPDEVETNCESWASFCFOKAOLKSANTGNRIINVSIKKKKPPSTNAGRQKRL 120

Qy	Db
121	121
TCPCSDSYKKPKPEFLERFKSLLOKMIHQHLSRTGSEDS	TCPCSDSYKKPKPEFLERFKSLLOKMIHQHLSRTGSEDS
162	162

RESULT 8
US-10-659-684-2
; Sequence 2, Application US/10659684
; Publication No. US20040110932A1

```

: GENERAL INFORMATION:
: APPLICANT: Novak, Julia E.
: APPLICANT: Preenell, Scott R.
: APPLICANT: Sprecher, Cindy A.
: APPLICANT: Foster, Donald C.
: APPLICANT: Holly, Richard D.
: APPLICANT: Gross, Jane A.
: APPLICANT: Johnston, Janet V.
: APPLICANT: Nelson, Andrew J.
: APPLICANT: Dillon, Stacey R.
: APPLICANT: Hammond, Angela K.
: TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
: FILE REFERENCE: 99-16

```

; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-659-684-2

Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGMERIVICLWYIFGLTVHKSSSGQGDHMI RMQLIDIVQLKNYVNDLVPEF 60
DB 1 MRSSPGMERIVICLWYIFGLTVHKSSSGQGDHMI RMQLIDIVQLKNYVNDLVPEF 60
QY 61 LPADEVETNCESAFSCFOQAOLKSANTGNNEIINVS IKLKRKPSTNAGRORHRL 120
DB 61 LPADEVETNCESAFSCFOQAOLKSANTGNNEIINVS IKLKRKPSTNAGRORHRL 120
QY 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 9
US-10-620-169-2
Sequence 2, Application US/10620169
Publication No. US20040136954A1
GENERAL INFORMATION:
APPLICANT: Grubby, Michael J
APPLICANT: Wuester, Andrea
APPLICANT: Young, Deborah
APPLICANT: Collins, Mary
APPLICANT: Whiters, Matthew
TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
FILE REFERENCE: 22058-585
CURRENT APPLICATION NUMBER: US/10/620,169
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/396,160
PRIOR FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/403,001
PRIOR FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-620-169-2

Query Match 100.0%; Score 850; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGMERIVICLWYIFGLTVHKSSSGQGDHMI RMQLIDIVQLKNYVNDLVPEF 60
DB 1 MRSSPGMERIVICLWYIFGLTVHKSSSGQGDHMI RMQLIDIVQLKNYVNDLVPEF 60
QY 61 LPADEVETNCESAFSCFOQAOLKSANTGNNEIINVS IKLKRKPSTNAGRORHRL 120
DB 61 LPADEVETNCESAFSCFOQAOLKSANTGNNEIINVS IKLKRKPSTNAGRORHRL 120
QY 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 10
US-10-872-087-10

Sequence 10, Application US/10872087
Publication No. US20040235743A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Novak, Julia E.
APPLICANT: West, James W.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA1 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22D1
CURRENT APPLICATION NUMBER: US/10/872,087
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 09/825,561
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-872-087-10

Query Match 100.0%; Score 850; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81; Indels 0; Gaps 0;
Matches 162; Conservative 0; Mismatches 0;

QY 1 MRSSPGMERIVICLWYIFGLTVHKSSSGQGDHMI RMQLIDIVQLKNYVNDLVPEF 60
DB 1 MRSSPGMERIVICLWYIFGLTVHKSSSGQGDHMI RMQLIDIVQLKNYVNDLVPEF 60
QY 61 LPADEVETNCESAFSCFOQAOLKSANTGNNEIINVS IKLKRKPSTNAGRORHRL 120
DB 61 LPADEVETNCESAFSCFOQAOLKSANTGNNEIINVS IKLKRKPSTNAGRORHRL 120
QY 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 11
US-10-787-442-2
Sequence 2, Application US/10787442
Publication No. US20040260065A1
GENERAL INFORMATION:
APPLICANT: Novak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/787,442
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,504
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2

LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-787-442-2

Query Match 100.0%; Score 850; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQODRHIMRMQLIDIVDQKYNVNDLVPER 60
DB 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQODRHIMRMQLIDIVDQKYNVNDLVPER 60
QY 61 LPAPDEVETNCESAFSCFOKQOLKSANTGNNERIINVSIKKLKRKPPSTNAGRQGRHL 120
DB 61 LPAPDEVETNCESAFSCFOKQOLKSANTGNNERIINVSIKKLKRKPPSTNAGRQGRHL 120
QY 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 12
US-10-951-239-2
Sequence 2, Application US/10951239
Publication No. US20050095223A1
GENERAL INFORMATION:
APPLICANT: Sivakumar, Pallavur
APPLICANT: Nelson, Andrew
TITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES
FILE REFERENCE: 03-09
CURRENT APPLICATION NUMBER: US/10/951,239
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: 60/505,919
PRIOR FILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-951-239-2

Query Match 100.0%; Score 850; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQODRHIMRMQLIDIVDQKYNVNDLVPER 60
DB 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQODRHIMRMQLIDIVDQKYNVNDLVPER 60
QY 61 LPAPDEVETNCESAFSCFOKQOLKSANTGNNERIINVSIKKLKRKPPSTNAGRQGRHL 120
DB 61 LPAPDEVETNCESAFSCFOKQOLKSANTGNNERIINVSIKKLKRKPPSTNAGRQGRHL 120
QY 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 13
US-10-775-204-2177
Sequence 2177, Application US/10775204
Publication No. US20050186664A1
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Haseltine, William A.
APPLICANT: Balance, David J.
APPLICANT: Turner, Andrew J.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF564
CURRENT APPLICATION NUMBER: US/10/775,204

CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/341,811
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/360,000
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/378,950
PRIOR FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 60/398,008
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: 60/411,355
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/414,984
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
PRIOR FILING DATE: 2002-01-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2177
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-2177

Query Match 100.0%; Score 850; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQODRHIMRMQLIDIVDQKYNVNDLVPER 60
DB 1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQODRHIMRMQLIDIVDQKYNVNDLVPER 60
QY 61 LPAPDEVETNCESAFSCFOKQOLKSANTGNNERIINVSIKKLKRKPPSTNAGRQGRHL 120
DB 61 LPAPDEVETNCESAFSCFOKQOLKSANTGNNERIINVSIKKLKRKPPSTNAGRQGRHL 120
QY 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 14
US-11-174-398-2
Sequence 2, Application US/11174398
Publication No. US20050244930A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: Novak, Julia E.
TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/11/174,398
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US/10/282,622
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-11-174-398-2

Query Match 100.0%; Score 850; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 2e-81;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSSPGNMERIVICLMTIFLGTLVHKSSGQODRHMRMROLIDIVDLKYYVNDLVPEF 60

Db 1 MRSSPGNMERIVICLMTIFLGTLVHKSSGQODRHMRMROLIDIVDLKYYVNDLVPEF 60

Qy 61 LPAPEDETNCENSAFSCFQKAOUKSANTGNNERIIIVSIIKLRKPPSTNAGRQKRL 120

Db 61 LPAPEDETNCENSAFSCFQKAOUKSANTGNNERIIIVSIIKLRKPPSTNAGRQKRL 120

Qy 121 TCPSCDSEYKPKPEFLERFKSLQKMIHOHLSRTHGSEDS 162

Db 121 TCPSCDSEYKPKPEFLERFKSLQKMIHOHLSRTHGSEDS 162

RESULT 15

US-11-134-489-2

; Sequence 2, Application US/11134489

; Publication No. US20050265966A1

; GENERAL INFORMATION:

; APPLICANT: Kindsvogel, Wayne R.

; APPLICANT: Hughes, Steven D.

; APPLICANT: Holly, Richard D.

; APPLICANT: Clegg, Christopher H.

; APPLICANT: Foster, Donald C.

; APPLICANT: Johnson, Rebecca A.

; APPLICANT: Hapel, Mark D.

; APPLICANT: Sivakumar, Pallavur V.

; TITLE OF INVENTION: METHODS OF TREATING CANCER USING IL-21 AND MONOCLONAL ANTIBODY TH

; FILE REFERENCE: 04-03

; CURRENT APPLICATION NUMBER: US/11/134,489

; CURRENT FILING DATE: 2005-05-20

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 162

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-134-489-2

Query Match 100.0%; Score 850; DB 6; Length 162;

Best Local Similarity 100.0%; Pred. No. 2e-81;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRSSPGNMERIVICLMTIFLGTLVHKSSGQODRHMRMROLIDIVDLKYYVNDLVPEF 60

Db 1 MRSSPGNMERIVICLMTIFLGTLVHKSSGQODRHMRMROLIDIVDLKYYVNDLVPEF 60

Qy 61 LPAPEDETNCENSAFSCFQKAOUKSANTGNNERIIIVSIIKLRKPPSTNAGRQKRL 120

Db 61 LPAPEDETNCENSAFSCFQKAOUKSANTGNNERIIIVSIIKLRKPPSTNAGRQKRL 120

Qy 121 TCPSCDSEYKPKPEFLERFKSLQKMIHOHLSRTHGSEDS 162

Db 121 TCPSCDSEYKPKPEFLERFKSLQKMIHOHLSRTHGSEDS 162

Search completed: September 7, 2006, 12:57:58
Job time : 59.2829 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:53:56 ; Search time 9.95143 Seconds
(without alignments)
1143.601 Million cell updates/sec

Title: US-10-659-684-2
Sequence: 1 MRSSPGNMERIVICLWIFL.....LLQKMIHQHLSRTGSEDS 162

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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2: /EMC_Celerra_SIDS3/prodata/1/pubppa/US06_NEW_PUB.pep.*
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7: /EMC_Celerra_SIDS3/prodata/1/pubppa/US11_NEW_PUB.pep.*
8: /EMC_Celerra_SIDS3/prodata/1/pubppa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	850	100.0	162	US-10-511-937-2572	Sequence 2572, Ap
2	850	100.0	162	US-10-735-149-2	Sequence 2, Appl
3	850	100.0	162	US-10-806-611-10	Sequence 10, Appl
4	850	100.0	162	US-11-429-276-2177	Sequence 2177, Ap
5	708.5	83.4	174	US-11-429-276-2167	Sequence 2167, Ap
6	706	83.1	134	US-10-735-149-28	Sequence 28, Appl
7	695	81.8	131	US-10-806-611-2	Sequence 2, Appl
8	524	61.6	122	US-10-806-611-12	Sequence 12, Appl
9	486	57.2	146	US-10-806-611-13	Sequence 13, Appl
10	394	46.4	122	US-10-806-611-4	Sequence 4, Appl
11	99.5	11.7	162	US-10-511-937-2499	Sequence 2499, Ap
12	82	9.6	605	US-11-429-276-1162	Sequence 1162, Ap
13	76.5	9.0	864	US-11-251-208-77	Sequence 77, Appl
14	74.5	8.8	431	US-11-056-355B-36356	Sequence 36356, A
15	74.5	8.8	431	US-11-056-355B-45283	Sequence 45283, A
16	74.5	8.8	441	US-11-056-355B-36355	Sequence 36355, A
17	74.5	8.8	441	US-11-056-355B-45282	Sequence 45282, A
18	74.5	8.8	463	US-11-056-355B-45281	Sequence 45281, A
19	74.5	8.8	463	US-11-056-355B-45281	Sequence 45281, A
20	74.5	8.8	1166	US-10-449-902-37528	Sequence 37528, A
21	73.5	8.6	466	US-10-953-349-18970	Sequence 18970, A
22	73.5	8.6	466	US-10-953-349-18969	Sequence 18969, A
23	73.5	8.6	565	US-10-471-571A-5038	Sequence 5038, Ap
24	71	8.4	378	US-10-953-349-32621	Sequence 32621, A
25	71	8.4	378	US-11-056-355B-64212	Sequence 64212, A

26	71	8.4	436	US-10-953-349-32620	Sequence 32620, A
27	71	8.4	436	US-11-056-355B-64211	Sequence 64211, A
28	71	8.4	461	US-10-953-349-32619	Sequence 32619, A
29	71	8.4	461	US-11-056-355B-64210	Sequence 64210, A
30	71	8.4	555	US-11-056-355B-79971	Sequence 79971, A
31	71	8.4	631	US-11-056-355B-79970	Sequence 79970, A
32	71	8.4	694	US-10-449-902-36372	Sequence 36372, A
33	71	8.4	864	US-11-056-355B-79969	Sequence 79969, A
34	70.5	8.3	352	US-11-056-355B-81843	Sequence 81843, A
35	70.5	8.3	720	US-10-449-902-51542	Sequence 51542, A
36	70	8.2	861	US-10-520-470-73	Sequence 73, Appl
37	69.5	8.2	653	US-10-449-902-52519	Sequence 52519, A
38	69	8.1	707	US-11-293-697-3241	Sequence 3241, Ap
39	69	8.1	923	US-10-449-902-41603	Sequence 41603, A
40	69	8.1	932	US-11-360-995-17	Sequence 17, Appl
41	69	8.1	932	US-11-360-995-18	Sequence 18, Appl
42	68.5	8.1	212	US-11-056-355B-4865	Sequence 4865, Ap
43	68.5	8.1	247	US-11-056-355B-56995	Sequence 56995, A
44	68.5	8.1	335	US-11-056-355B-4864	Sequence 4864, Ap
45	68.5	8.1	417	US-11-056-355B-4863	Sequence 4863, Ap

ALIGNMENTS

RESULT 1
US-10-511-937-2572
Sequence 2572, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wollgmut, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511.937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2572
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2572

Query Match 100.0%; Score 850; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSPGNMERIVICLWIFLGTIVHKSSGQGDHRMIRKQLIDIVOLKNYVNDLYPEF 60
DB 1 MRSSPGNMERIVICLWIFLGTIVHKSSGQGDHRMIRKQLIDIVOLKNYVNDLYPEF 60
DB LPAPEDVETNCESAFSCFOAKOLKSANTGNNEIIVASTIKLKRKPPSTNAGRORHRL 120
QY 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162
DB 121 TCPSCDSEYKKPKPEFLERFKSLQKMIHQHLSRTGSEDS 162

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RESULT 2
US-10-735-149-2
; Sequence 2, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Cover, Bruce L.
; APPLICANT: Cover, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-735-149-2

Query Match      100.0%; Score 850; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQGDHMRIRMQLDIVDQKNYVNDLVPEF 60
Db      1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQGDHMRIRMQLDIVDQKNYVNDLVPEF 60

Qy      61 LPAPDEVETNCESAFSCFOKAQLKSANTGNNERIINVSISKLRKPPSTNAGRQKHRL 120
Db      61 LPAPDEVETNCESAFSCFOKAQLKSANTGNNERIINVSISKLRKPPSTNAGRQKHRL 120

Qy      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

Qy      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 3
US-10-806-611-10
; Sequence 10, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chiu, Elaine Y.
; APPLICANT: Senices, Mayra A.
; APPLICANT: Young, Deborah A.
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
; FILE REFERENCE: 16158-013001
; CURRENT APPLICATION NUMBER: US/10/806,611
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 60/456,920
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-611-10

Query Match      100.0%; Score 850; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQGDHMRIRMQLDIVDQKNYVNDLVPEF 60
Db      1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQGDHMRIRMQLDIVDQKNYVNDLVPEF 60

Qy      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

Qy      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
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Db      1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQGDHMRIRMQLDIVDQKNYVNDLVPEF 60
Qy      61 LPAPDEVETNCESAFSCFOKAQLKSANTGNNERIINVSISKLRKPPSTNAGRQKHRL 120
Db      61 LPAPDEVETNCESAFSCFOKAQLKSANTGNNERIINVSISKLRKPPSTNAGRQKHRL 120

Qy      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 4
US-11-429-276-2177
; Sequence 2177, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2177
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-2177

Query Match      100.0%; Score 850; DB 7; Length 162;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQGDHMRIRMQLDIVDQKNYVNDLVPEF 60
Db      1 MRSSPGNMERIVICLWVIFLGLTVHKSSSGQGDHMRIRMQLDIVDQKNYVNDLVPEF 60

Qy      61 LPAPDEVETNCESAFSCFOKAQLKSANTGNNERIINVSISKLRKPPSTNAGRQKHRL 120
Db      61 LPAPDEVETNCESAFSCFOKAQLKSANTGNNERIINVSISKLRKPPSTNAGRQKHRL 120

Qy      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162
Db      121 TCPSCDSEYKPKPEFLERFKSLQKMIHQHLSRTHGSEDS 162

RESULT 5
US-11-429-276-2167
; Sequence 2167, Application US/11429276
; Publication No. US20060194735A1
; GENERAL INFORMATION:
; APPLICANT: Roosen et al.
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;; TITLE OF INVENTION: Albumin Fusion Proteins
;; FILE REFERENCE: PFS64
;; CURRENT APPLICATION NUMBER: US/11/429,276
;; CURRENT FILING DATE: 2006-05-08
;; PRIOR APPLICATION NUMBER: 10/775,204
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: PCT/US02/40891
;; PRIOR FILING DATE: 2002-12-23
;; PRIOR APPLICATION NUMBER: 60/341,811
;; PRIOR FILING DATE: 2001-12-21
;; PRIOR APPLICATION NUMBER: 60/360,000
;; PRIOR FILING DATE: 2002-02-28
;; PRIOR APPLICATION NUMBER: 60/378,950
;; PRIOR FILING DATE: 2002-05-10
;; PRIOR APPLICATION NUMBER: 60/398,008
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;; PRIOR FILING DATE: 2002-09-18
;; PRIOR APPLICATION NUMBER: 60/414,984
;; PRIOR FILING DATE: 2002-10-02
;; PRIOR APPLICATION NUMBER: 60/417,611
;; PRIOR FILING DATE: 2002-10-11
;; PRIOR APPLICATION NUMBER: 60/420,246
;; PRIOR FILING DATE: 2002-10-23
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 2222
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2167
;; LENGTH: 742
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-429-276-2167

Query Match 83.4%; Score 708.5; DB 7; Length 742;
Best Local Similarity 90.1%; Pred. No. 2e-60;
Matches 136; Conservative 5; Mismatches 7; Indels 3; Gaps 1;
QY 15 LMTVFLGLTVHKS---SGGDRHMIRKRLIDVDLQKYNVNDLVPEFLPAPEDVETNC 71
DB 7 ISLFLFSSAYSRSIDRKQGGDRHMIRKRLIDVDLQKYNVNDLVPEFLPAPEDVETNC 66
QY 72 EWSAFSCGQKQKLSANTGNNERIINVSIKLKRPSTNAGRQKRLTGPCSDSYEKK 131
DB 67 EWSAFSCGQKQKLSANTGNNERIINVSIKLKRPSTNAGRQKRLTGPCSDSYEKK 126
QY 132 PKKEFLERFKSLQKMIHQHLSRTHGSEDS 162
DB 127 PKKEFLERFKSLQKMIHQHLSRTHGSEDS 157

RESULT 6
US-10-735-149-28
;; Sequence 28, Application US/10735149
;; Publication No. US20060134754A1
;; GENERAL INFORMATION:
;; APPLICANT: Chan, Chung
;; APPLICANT: Zamosc, Bruce L.
;; APPLICANT: Covert, Douglas C.
;; APPLICANT: Liu, Hong Y.
;; APPLICANT: De Jongh, Karen S.
;; APPLICANT: Meyer, Jeffrey D.
;; APPLICANT: Holderman, Susan D.
;; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
;; FILE REFERENCE: 02-12
;; CURRENT APPLICATION NUMBER: US/10/735,149
;; CURRENT FILING DATE: 2003-12-12
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 28
;; LENGTH: 134
;; TYPE: PRT
;; ORGANISM: Artificial Sequence

;; FEATURE:
;; OTHER INFORMATION: optimized IL-21
US-10-735-149-28

Query Match 83.1%; Score 706; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 4.2e-61;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 QGDRHMIRKRLIDVDLQKYNVNDLVPEFLPAPEDVETNCWSAFSCFOKQKLSANT 89
DB 2 QGDRHMIRKRLIDVDLQKYNVNDLVPEFLPAPEDVETNCWSAFSCFOKQKLSANT 61
QY 90 GNNERIINVSIKLKRPSTNAGRQKRLTGPCSDSYEKKPKPEFLERFKSLQKMIH 149
DB 62 GNNERIINVSIKLKRPSTNAGRQKRLTGPCSDSYEKKPKPEFLERFKSLQKMIH 121
QY 150 QHLSRTHGSEDS 162
DB 122 QHLSRTHGSEDS 134

RESULT 7
US-10-806-611-2
;; Sequence 2, Application US/10806611
;; Publication No. US20060159655A1
;; GENERAL INFORMATION:
;; APPLICANT: Collins, Mary
;; APPLICANT: Chin, Elaine Y.
;; APPLICANT: Senices, Mayra
;; APPLICANT: Young, Deborah A.
;; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
;; FILE REFERENCE: 16158-013001
;; CURRENT APPLICATION NUMBER: US/10/806,611
;; CURRENT FILING DATE: 2004-03-22
;; PRIOR APPLICATION NUMBER: US 60/456,920
;; PRIOR FILING DATE: 2003-03-21
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 2
;; LENGTH: 131
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-806-611-2

Query Match 81.8%; Score 695; DB 6; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.8e-60;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 QDRHMIRKRLIDVDLQKYNVNDLVPEFLPAPEDVETNCWSAFSCFOKQKLSANTGN 91
DB 1 QDRHMIRKRLIDVDLQKYNVNDLVPEFLPAPEDVETNCWSAFSCFOKQKLSANTGN 60
QY 92 NERIINVSIKLKRPSTNAGRQKRLTGPCSDSYEKKPKPEFLERFKSLQKMIHQH 151
DB 61 NERIINVSIKLKRPSTNAGRQKRLTGPCSDSYEKKPKPEFLERFKSLQKMIHQH 120
QY 152 LSSRTHGSEDS 162
DB 121 LSSRTHGSEDS 131

RESULT 8
US-10-806-611-12
;; Sequence 12, Application US/10806611
;; Publication No. US20060159655A1
;; GENERAL INFORMATION:
;; APPLICANT: Collins, Mary
;; APPLICANT: Chin, Elaine Y.
;; APPLICANT: Senices, Mayra
;; APPLICANT: Young, Deborah A.
;; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
;; TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR

FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 122
TYPE: PRT
ORGANISM: Bos taurus
US-10-806-611-12

Query Match 61.6%; Score 524; DB 6; Length 122;
Best Local Similarity 80.3%; Pred. No. 1.5e-43;
Matches 98; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 32 QDRHIMRQLIDVDOLKNNVNDLVEPEFLPAPEDVETNCWSAFSCFOKAQLKSANTGN 91
DB 1 QDRFLIRQLIDVDOLKNNVNDLVEPEFLPAPEDVETNCWSAFSCFOKAQLKSANTGN 60
QY 92 NERINVSIKKLKRPSTNAGRQKRLTCSYCKPKPEFLERFKSLQKMIHQH 151
DB 61 NEKINILTKQLKRLPATWTGRQKHVETPCSDSYCKPKPEFLERFKSLQKMIHQH 120
QY 152 LS 153
DB 121 LS 122

RESULT 9
US-10-806-611-13
Sequence 13, Application US/10806611
Publication No. US20060159655A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 146
TYPE: PRT
ORGANISM: Mus musculus
US-10-806-611-13

Query Match 57.2%; Score 486; DB 6; Length 146;
Best Local Similarity 63.0%; Pred. No. 8.9e-40;
Matches 92; Conservative 23; Mismatches 31; Indels 0; Gaps 0;

QY 8 MERIVICLWYIFLGTLVHKSSQGDHMIIMRQLIDVDOLKNNVNDLVEPEFLPAPEDV 67
DB 1 MERVLVCLVYIFLGTLVHKSSQGDHMIIMRQLIDVDOLKNNVNDLVEPEFLPAPEDV 60
QY 68 ETNCWSAFSCFOKAQLKSANTGNNERINVSIKKLKRPSTNAGRQKRLTCSYCK 127
DB 61 KGCHEHAFAFCFOKAKKRPSPNGNKTFFILDVQLRRRLPARGGKKQKXIAKCPSCDS 120
QY 128 YEKKPKPEFLERFKSLQKMIHQHLS 153
DB 121 YEKTPKEFLERFKSLQKMIHQHLS 146

RESULT 10
US-10-806-611-4

Sequence 4, Application US/10806611
Publication No. US20060159655A1
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Chin, Elaine Y.
APPLICANT: Senices, Mayra
APPLICANT: Young, Deborah A.
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
FILE REFERENCE: 16158-013001
CURRENT APPLICATION NUMBER: US/10/806,611
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: US 60/456,920
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 122
TYPE: PRT
ORGANISM: Mus musculus
US-10-806-611-4

Query Match 46.4%; Score 394; DB 6; Length 122;
Best Local Similarity 62.0%; Pred. No. 5.7e-31;
Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 33 DRHIMRQLIDVDOLKNNVNDLVEPEFLPAPEDVETNCWSAFSCFOKAQLKSANTGN 92
DB 2 DRILIRLRLIDIVEQLKTYENDLPELSPQDVKGCHHAFAFCFOKAKKLPSPNGN 61
QY 93 ERIINVSIKKLKRPSTNAGRQKRLTCSYCKPKPEFLERFKSLQKMIHQH 152
DB 62 KTFILDLVQLRRRLPARRGKKQKXIAKCPSCDSYCKPKPEFLERFKSLQKMIHQH 121
QY 153 S 153
DB 122 S 122

RESULT 11
US-10-511-937-2499
Sequence 2499, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Monigemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2499
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2499

Query Match 11.7%; Score 99.5; DB 6; Length 162;
Best Local Similarity 25.9%; Pred. No. 0.025;

OTHER INFORMATION: Ceres Seq. ID no. 13575998
US-11-056-355B-36356

Query Match 8.8%; Score 74.5; DB 7; Length 431;
Best Local Similarity 21.8%; Pred. No. 22;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY 34 RHMIRMQLDIVDQKNYVNDLVPEFLPAPEDVETNCWMSAFSCFOKAOLKSANTGNNE 93
DB 220 KYKLAARKFLDVNPGLGNSYNEVI----APQDIATYGGLCALASFDRSEIK-----Q 267
QY 94 RII-NVSIKIKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPPKEFLERFKSLQKMIHQH 151
DB 268 KVIDINIFRNFLVLPVRELINDFYSSRYASC-----LEYLASIKSNLLLDIH 318

RESULT 15

US-11-056-355B-45283
; Sequence 45283, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION: Brover, Vyacheslav
; APPLICANT: Alexander, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ. ID NOS: 119966
; SEQ. ID NO 45283
; LENGTH: 431
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(431)
; OTHER INFORMATION: Ceres Seq. ID no. 13575998
US-11-056-355B-45283

Query Match 8.8%; Score 74.5; DB 7; Length 431;
Best Local Similarity 21.8%; Pred. No. 22;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY 34 RHMIRMQLDIVDQKNYVNDLVPEFLPAPEDVETNCWMSAFSCFOKAOLKSANTGNNE 93
DB 220 KYKLAARKFLDVNPGLGNSYNEVI----APQDIATYGGLCALASFDRSEIK-----Q 267
QY 94 RII-NVSIKIKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPPKEFLERFKSLQKMIHQH 151
DB 268 KVIDINIFRNFLVLPVRELINDFYSSRYASC-----LEYLASIKSNLLLDIH 318

Search completed: September 7, 2006, 12:58:48
Job time : 10.9514 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:39:36 : Search time 222.886 Seconds
(without alignments)
1103.626 Million cell updates/sec

Title: US-10-659-684-115

Perfect score: 2958

Sequence: 1 MPRGMAAPLLLLLLQGSGWC.....YLRQWVTPPLSPSPQAS 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapect 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2958	100.0	538	2 AAY27450	Aay27450 Human MU-
2	2958	100.0	538	3 AAB18634	Aab18634 A human z
3	2958	100.0	538	3 AAY45031	Aay45031 HUMAN Crp
4	2958	100.0	538	3 AAY69886	Aay69886 Human hae
5	2958	100.0	538	3 AAY79312	Aay79312 Human cyt
6	2958	100.0	538	4 AAB48001	Aab48001 Human IL-
7	2958	100.0	538	5 ABB81960	Abb81960 Human 164
8	2958	100.0	538	5 AAU11912	Aau11912 Human MU-
9	2958	100.0	538	5 AAU11912	Aau11912 Human MU-
10	2958	100.0	538	5 AAU11978	Aau11978 Human sol
11	2958	100.0	538	6 ABR61402	Abr61402 Human IL-
12	2958	100.0	538	7 AAE14939	Aae14939 Human int
13	2958	100.0	538	7 ABU62888	Abu62888 Human MU-
14	2958	100.0	538	7 ABW00881	Abw00881 Human cyt
15	2958	100.0	538	7 ADG87460	Adg87460 Human zai
16	2958	100.0	538	7 ADH44685	Adh44685 Human zai
17	2958	100.0	538	7 ADI01021	Adi01021 Immunity-
18	2958	100.0	538	8 ADH10505	Adh10505 Human int
19	2958	100.0	538	8 ADJ25623	Adj25623 Human int
20	2958	100.0	538	8 ADM83456	Adm83456 Human zai
21	2958	100.0	538	8 ADL91861	Adl91861 Human PRO
22	2958	100.0	538	8 ADP19844	Adp19844 Human zai
23	2958	100.0	538	8 ADS82585	Ads82585 Interleuk

24	2958	100.0	538	8 ADS19027	Ads19027 Mature hu
25	2958	100.0	538	8 ADS41470	Ads41470 Human hae
26	2958	100.0	538	8 ADV96468	Adv96468 Human rec
27	2958	100.0	538	9 ADY17832	Ady17832 PRO polyp
28	2958	100.0	538	9 ADY17690	Ady17690 PRO polyp
29	2958	100.0	538	9 ADY20089	Ady20089 PRO polyp
30	2958	100.0	538	9 ADY54732	Ady54732 Human zai
31	2958	100.0	538	9 ADY21785	Ady21785 Human can
32	2958	100.0	538	9 ADZ12787	Adz12787 Human can
33	2958	100.0	538	9 ADZ20509	Adz20509 Human int
34	2958	100.0	538	10 AEE19676	Aee19676 Human int
35	2958	100.0	538	10 AEG05256	Aeg05256 Human IL-
36	2951	99.8	538	3 AAY94304	Aay94304 Human HNO
37	2951	99.8	538	4 AAU08728	Aau08728 Human HNO
38	2933	99.2	538	4 AAB02459	Aab02459 Human DNA
39	2905	98.2	538	3 AAY69888	Aay69888 Mouse hae
40	2851	96.4	519	9 ADY54825	Ady54825 Human zai
41	2817	95.2	568	3 AAY94305	Aay94305 Human HNO
42	2817	95.2	568	4 AAEO2457	Aae02457 Human DNA
43	2817	95.2	568	4 AAU08729	Aau08729 Human HNO
44	2817	95.2	568	5 AAE13738	Aae13738 Human sol
45	1899.5	64.2	361	3 AAY69883	Aay69883 Human hae

ALIGNMENTS

RESULT 1
ID AAY27450 standard; protein; 538 AA.
XX
AC AAY27450;
XX
DT 26-NOV-1999 (first entry)
XX
DE Human MU-1 hematopoietin receptor protein.
XX
KW MU-1 hematopoietin receptor protein; e MU-1 protein; gene therapy;
KW cell proliferation; cytokine production; immune response; cancer;
KW autoimmune disease; transplant rejection; hematopoiesis; anemia;
KW gene mapping; nutritional supplement; human.
XX
OS Homo sapiens.
XX
PN W09947675-A1.
XX
PD 23-SEP-1999.
XX
PF 17-MAR-1999; 99MO-US005854.
XX
PR 17-MAR-1998; 98US-00040005.
XX
PA (GEMV) GENETICS INST INC.
XX
PI Donaldson D, Ungar M;
XX WPI, 1999-562115/47.
XX DR N-PSDB; AAZ07535.
XX PT New nucleic acid encoding the MU-1 hematopoietin receptor protein, used
XX for treating e.g. cancer, autoimmune disease or abnormal hematopoiesis.
XX
XX Claim 9, Page 33-35; 37pp; English.
XX
XX This represents a MU-1 hematopoietin receptor protein. The protein can be
XX produced by standard recombinant methodology. The MU-1 protein has the
XX biological activity of the MU-1 hematopoietin receptor superfamily chain.
XX It is used to screen for specific binding agents, to raise specific
XX antibodies, as assay reagents, tissue markers etc. and therapeutically
XX (optionally) expressed from the MU-1 gene by gene therapy. Many possible
XX activities/uses of the MU-1 protein are described without supporting
XX evidence, e.g. they regulate cell proliferation and differentiation,
XX induce production of cytokines, stimulate or suppress an immune response

CC (e.g. for treating immune deficiency of any etiology, cancer or
 CC autoimmune disease, and for preventing transplant rejection) and regulate
 CC of hematopoiesis, e.g. for treating anemia. The MU-1 gene is used as a
 CC research reagent, for recombinant production of the protein, as tissue or
 CC molecular weight marker, for gene mapping; for production of anti-DNA or
 CC anti-protein antibodies etc. The MU-1 protein and the nucleic acids are
 CC also useful as nutritional supplements or sources and the antibodies can
 CC be used therapeutically, as assay reagents and for affinity purification
 CC
 XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 2; Length 538;
 Best Local Similarity 100.0%; Pred. No. 7.5e-240; Indels 0; Gaps 0;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLILLLLLOGMGCPDLVCYTDYLOTVCILEMNNLHPSTLTTLTWMQDYEELKD 60
 DB 1 MPRGMAAPLILLLLLOGMGCPDLVCYTDYLOTVCILEMNNLHPSTLTTLTWMQDYEELKD 60
 QY 61 EATSCSLHRSAHNATHATYTCMDVFFHMADDFSVNITDQSGNYSQECGFLAIESIKP 120
 DB 61 EATSCSLHRSAHNATHATYTCMDVFFHMADDFSVNITDQSGNYSQECGFLAIESIKP 120
 QY 121 APPNVTVTSSGOYNISWRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
 DB 121 APPNVTVTSSGOYNISWRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
 QY 181 RSVSLPLERFKDSSYELQVRAGMPGSSYOGTSEMSDPVIFOTOSSEELKEGNPHLL 240
 DB 181 RSVSLPLERFKDSSYELQVRAGMPGSSYOGTSEMSDPVIFOTOSSEELKEGNPHLL 240
 QY 241 LLLLVIVIFPAFWSLKTHTPLRLMKKIWA VSPERFFMPLKYKCGSDPKKVVGA PFTGSS 300
 DB 241 LLLLVIVIFPAFWSLKTHTPLRLMKKIWA VSPERFFMPLKYKCGSDPKKVVGA PFTGSS 300
 QY 301 LELGPMSPPEVSTLEVYSCHPRSPAKRLQLTLOEPALVESDGVKPSFWPTAONSGG 360
 DB 301 LELGPMSPPEVSTLEVYSCHPRSPAKRLQLTLOEPALVESDGVKPSFWPTAONSGG 360
 QY 361 SAYSEERDRPYGLVSDITVTVLDABEGPCTWPCSCEDDGYPALDLDAGLESPGLEDEPLLD 420
 DB 361 SAYSEERDRPYGLVSDITVTVLDABEGPCTWPCSCEDDGYPALDLDAGLESPGLEDEPLLD 420
 QY 421 AGTTVLSGCGVSAGSPGLGPGLSLDRKPLADGEMAGGLPMGGRSPGCVSESEAGS 480
 DB 421 AGTTVLSGCGVSAGSPGLGPGLSLDRKPLADGEMAGGLPMGGRSPGCVSESEAGS 480
 QY 481 PLAGLMDPTDFSGVSGSPVCECDFTSPGDEGPPRSYLQWVVIPIPLSSPGQAS 538
 DB 481 PLAGLMDPTDFSGVSGSPVCECDFTSPGDEGPPRSYLQWVVIPIPLSSPGQAS 538

RESULT 2

AAAB18634
 ID AAB18634 standard; protein. 538 AA.

AC AAB18634;

DT 22-JAN-2001 (first entry)

DE A human zalphall ligand polypeptide.

XX zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;

XX tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

XX Homo sapiens.

PN W0200053761-A2.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000WO-US006067.

XX

PR 09-MAR-1999; 99US-00264908.
 PR 11-MAR-1999; 99US-00265992.
 PR 01-JUL-1999; 99US-0142013P.
 PA (ZYMO) ZYMOGENETICS INC.
 PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 DR WPI; 2000-565600/52.
 DR N-PSDB; AAA75557.
 XX
 PT New human cytokine, designated zalphall ligand, useful for stimulating
 PT the proliferation and/or development of hematopoietic cells in vitro and
 PT in vivo, and for treating tumorigenesis.
 PS Disclosure; Page 255-256; 256pp; English.

CC The present sequence represents a human zalphall ligand polypeptide,
 CC which is a cytokine. The zalphall ligand is useful for stimulating the
 CC proliferation and development of haematopoietic cells in vitro and in
 CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
 CC for cloning the zalphall gene. The zalphall ligand is useful for treating
 CC tumorigenesis. A zalphall ligand-saporin fusion toxin may be used for
 CC treating leukaemias and lymphomas. Antagonists against zalphall ligand
 CC are useful as research reagents for characterizing ligand-receptor
 CC interaction. Antagonists are also useful for inhibiting expansion,
 CC proliferation, activation and differentiation of cells involved in
 CC regulating hematopoiesis. The zalphall ligand may also be used to
 CC stimulate an immune response against B cell tumour, a virus, a parasite
 CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
 CC agonists and antibodies are also useful for the detection, diagnosis,
 CC prevention, and treatment of diseases associated with a zalphall ligand
 CC genetic defect
 CC
 XX

Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 3; Length 538;
 Best Local Similarity 100.0%; Pred. No. 7.5e-240; Indels 0; Gaps 0;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLILLLLLOGMGCPDLVCYTDYLOTVCILEMNNLHPSTLTTLTWMQDYEELKD 60
 DB 1 MPRGMAAPLILLLLLOGMGCPDLVCYTDYLOTVCILEMNNLHPSTLTTLTWMQDYEELKD 60
 QY 61 EATSCSLHRSAHNATHATYTCMDVFFHMADDFSVNITDQSGNYSQECGFLAIESIKP 120
 DB 61 EATSCSLHRSAHNATHATYTCMDVFFHMADDFSVNITDQSGNYSQECGFLAIESIKP 120
 QY 121 APPNVTVTSSGOYNISWRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
 DB 121 APPNVTVTSSGOYNISWRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
 QY 181 RSVSLPLERFKDSSYELQVRAGMPGSSYOGTSEMSDPVIFOTOSSEELKEGNPHLL 240
 DB 181 RSVSLPLERFKDSSYELQVRAGMPGSSYOGTSEMSDPVIFOTOSSEELKEGNPHLL 240
 QY 241 LLLLVIVIFPAFWSLKTHTPLRLMKKIWA VSPERFFMPLKYKCGSDPKKVVGA PFTGSS 300
 DB 241 LLLLVIVIFPAFWSLKTHTPLRLMKKIWA VSPERFFMPLKYKCGSDPKKVVGA PFTGSS 300
 QY 301 LELGPMSPPEVSTLEVYSCHPRSPAKRLQLTLOEPALVESDGVKPSFWPTAONSGG 360
 DB 301 LELGPMSPPEVSTLEVYSCHPRSPAKRLQLTLOEPALVESDGVKPSFWPTAONSGG 360
 QY 361 SAYSEERDRPYGLVSDITVTVLDABEGPCTWPCSCEDDGYPALDLDAGLESPGLEDEPLLD 420
 DB 361 SAYSEERDRPYGLVSDITVTVLDABEGPCTWPCSCEDDGYPALDLDAGLESPGLEDEPLLD 420
 QY 421 AGTTVLSGCGVSAGSPGLGPGLSLDRKPLADGEMAGGLPMGGRSPGCVSESEAGS 480
 DB 421 AGTTVLSGCGVSAGSPGLGPGLSLDRKPLADGEMAGGLPMGGRSPGCVSESEAGS 480

Qy 481 PLGLMDTDFDSGFGVSDCSSPVCEDTSPGDEGPPRSYLROWVVIIPPLSSPGPQAS 538
 Db 481 PLGLMDTDFDSGFGVSDCSSPVCEDTSPGDEGPPRSYLROWVVIIPPLSSPGPQAS 538

RESULT 3

AAV45031
 ID AAV45031 standard; protein; 538 AA.

AAV45031;

31-MAY-2000 (first entry)

HUMAN Orphan Cytokine Receptor 10 (OCR10) -A polypeptide.

Human; Orphan Cytokine Receptor 10-A; OCR10-A; cytokine; screen; cognate ligand; treatment; endocrine disorder; immune disorder.

Homo sapiens.

WC200008152-A1.

17-FEB-2000.

16-JUL-1999; 99MO-US016060.

04-AUG-1998; 98US-00128820.

(REG-) REGENERON PHARM INC.

Masiakowski PJ, Morris J, Valenzuela DM;

WPI; 2000-205707/18.

N-PSDB; AAZ50748.

New HUMAN orphan cytokine receptors 10 and 10-A useful for screening for drugs e.g. receptor agonists that may mediate survival and differentiation in cells naturally expressing the receptor and for screening for cognate ligands.

Example 10; Page 39-41; 54pp; English.

The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A (OCR10-A) polypeptide. It is expressed at high levels in spleen, thymus, peripheral blood leucocytes and lymph nodes and moderately in heart and placenta. It has a role in immune system and cytokine function. It is useful in screening for cognate ligands or drugs that mediate survival and differentiation of cells expressing this receptor. Modified HUMAN OCR10-A or its agonist can be used in the treatment of endocrine or immune disorders

Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 3; Length 538;

Best Local Similarity 100.0%; Pred. No. 7, 5e-240; Indels 0; Gaps 0;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYLTQTVCIEMNNLHPSTLTLTWQDYBELKD 60
 Db 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYLTQTVCIEMNNLHPSTLTLTWQDYBELKD 60
 Qy 61 EATSCSLHRSANNAHTATYTCMDVFPFMAADIFSVNITDQSGVSGEGSFLAESTIKP 120
 Db 61 EATSCSLHRSANNAHTATYTCMDVFPFMAADIFSVNITDQSGVSGEGSFLAESTIKP 120
 Qy 121 APPNNVVTSSGQVNIWSRSDYEDPAFYMLKGLQYELQYNNRCDPMAVSRRLKLSVDS 180
 Db 121 APPNNVVTSSGQVNIWSRSDYEDPAFYMLKGLQYELQYNNRCDPMAVSRRLKLSVDS 180
 Qy 181 RSVSLPLPEPKDSSYELQVAGPMPGSSYQGTWSEMSDPVI FOTOSBELREGNNPHLL 240
 Db 181 RSVSLPLPEPKDSSYELQVAGPMPGSSYQGTWSEMSDPVI FOTOSBELREGNNPHLL 240

Qy 241 LLLVIVFIPAFMSLKTHTPLMRLLKIMAVSPERFEMPLYKGGSGDFKKWVGAFTGSS 300
 Db 241 LLLVIVFIPAFMSLKTHTPLMRLLKIMAVSPERFEMPLYKGGSGDFKKWVGAFTGSS 300
 Qy 301 LEIGPMSPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVELVESDGVKPSFMP7AQN5G 360
 Db 301 LEIGPMSPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVELVESDGVKPSFMP7AQN5G 360
 Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCWPCSCCEDDYPALDLDAGLBP9GLDEPLD 420
 Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCWPCSCCEDDYPALDLDAGLBP9GLDEPLD 420
 Qy 421 AGTTVSCGVSAGSPGLGSLDRLKPLADGEDMAGGLPMGGRSPGVSE5AGS 480
 Db 421 AGTTVSCGVSAGSPGLGSLDRLKPLADGEDMAGGLPMGGRSPGVSE5AGS 480
 Qy 481 PLGLMDTDFDSGFGVSDCSSPVCEDTSPGDEGPPRSYLROWVVIIPPLSSPGPQAS 538
 Db 481 PLGLMDTDFDSGFGVSDCSSPVCEDTSPGDEGPPRSYLROWVVIIPPLSSPGPQAS 538

RESULT 4

AAV69886
 ID AAV69886 standard; protein; 538 AA.

AAV69886;

24-MAY-2000 (first entry)

Human haemopoietin receptor family member NR8gamma.

Haemopoietin receptor family; NR8; antibody; diagnosis;

blood formation disorder.

Homo sapiens.

WC200008152-A1.

29-DEC-1999.

23-JUN-1999; 99MO-JP003351.

24-JUN-1998; 98JP-00214720.

PR 19-OCT-1998; 98UP-00297409.

(CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.

Nomura H, Maeda M;

WPI; 2000-116933/10.

N-PSDB; AAZ59240.

Hemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders.

Claim 4; Fig 9-10; 176pp; Japanese.

This sequence represents a novel haemopoietin receptor protein family NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders

Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 3; Length 538;

Best Local Similarity 100.0%; Pred. No. 7, 5e-240; Indels 0; Gaps 0;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYLTQTVCIEMNNLHPSTLTLTWQDYBELKD 60
 Db 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYLTQTVCIEMNNLHPSTLTLTWQDYBELKD 60
 Qy 61 EATSCSLHRSANNAHTATYTCMDVFPFMAADIFSVNITDQSGVSGEGSFLAESTIKP 120

```

Db 61 EATSCSLHRSAHNATHATYTCHMDVFFHMADDFSVNITDQSGNYSGECCSFLAESTIKP 120
Qy 121 APPFNVTVTSSGQYNIWSRSDYEDPAFYMLKGKLYELOYRNKGDPMVAVSPRKRLISVDS 180
Db 121 APPFNVTVTSSGQYNIWSRSDYEDPAFYMLKGKLYELOYRNKGDPMVAVSPRKRLISVDS 180
Qy 181 RSVSLPLEFRKSSYELQVRAGPMPGSSYGQTSWSDPVIPTQOSEBELKEGMNPHLL 240
Db 181 RSVSLPLEFRKSSYELQVRAGPMPGSSYGQTSWSDPVIPTQOSEBELKEGMNPHLL 240
Qy 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWAVPSPERFPMPLKKGSGDFKKVAVGAPFTGSS 300
Db 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWAVPSPERFPMPLKKGSGDFKKVAVGAPFTGSS 300
Qy 301 LEIGPMSPERVSTLEVYSCHPPRSPAKRLQLTLEQEPALVESGCVKPSGFWPTAQNSSG 360
Db 301 LEIGPMSPERVSTLEVYSCHPPRSPAKRLQLTLEQEPALVESGCVKPSGFWPTAQNSSG 360
Qy 361 SAYSEERDPRYGLVSIPTVTVLDAEGPCTWPCSGEDDGYPALDIDAGLEPSGLJEDPLD 420
Db 361 SAYSEERDPRYGLVSIPTVTVLDAEGPCTWPCSGEDDGYPALDIDAGLEPSGLJEDPLD 420
Qy 421 AGTVLSCGCVSAGSPGLGSPGLDLRLKPLADGEDMAGCLPMGGRSPCGVSESEAGS 480
Db 421 AGTVLSCGCVSAGSPGLGSPGLDLRLKPLADGEDMAGCLPMGGRSPCGVSESEAGS 480
Qy 481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGQAS 538
Db 481 PLAGLMDTFDPSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIPLPSSPGQAS 538

```

RESULT 5
AAV79312

ID AAV79312 standard; protein, 538 AA.

XX AAV79312;

DT 18-JUL-2000 (first entry)

XX Human cytokine receptor zalphall.

XX Cytokine receptor; zalphall; human; chromosome 16p11.1; apoptosis;
KM signal transduction; growth factor; cancer; tumour; infection;
KM immunosuppressive; immunostimulant; autoimmune disease; leukaemia;
KM lymphoma; transplant rejection; therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19 /note= "signal peptide"

FT Protein 20..538 /note= "mature protein; a polypeptide comprising the mature protein is specifically claimed in Claim 27(d)"

FT Domain 20..237 /note= "cytokine-binding domain; a polypeptide comprising this domain is specifically claimed in Claim 27(a)"

FT Domain 192..202 /note= "penultimate strand region"

FT Region 214..218 /note= "MSXMS motif"

FT Domain 238..255 /note= "transmembrane domain"

FT Domain 256..538 /note= "intracellular signalling domain; a polypeptide comprising this domain is specifically claimed in Claim 27(c)"

FT Region 267..273 /note= "Box I signalling site"

FT Region 301..304 /note= "Box II signalling site"

FT Region

XX

PN WO200017235-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 99WO-US022149.
XX
PR 23-SEP-1998; 98US-00159254.
PR 09-MAR-1999; 99US-00265117.
PR 06-JUL-1999; 99US-00347930.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX
DR WPI: 2000-292825/25.
DR N-PSDB; AA294533, AA294534.
XX
PT Novel nucleic acid encoding zalphall polypeptide, useful for treating
PT e.g. viral infection or tumors, and for identifying ligands that
PT stimulate cell proliferation.
XX
PS Claim 27(e); Page 148-149; 190pp; English.

XX The present sequence is that of zalphall, a novel human class I cytokine
CC receptor that may be involved in an apoptotic cellular pathway, or is a
CC cell-cell signalling molecule, growth factor receptor, or extracellular
CC matrix associated protein with growth factor hormone activity. The
CC sequence was deduced from a cDNA clone (see AA294533) isolated from a
CC spinal cord library. Polypeptides comprising amino acids 20-237, 20-255,
CC 256-538, 20-538 and 1-538 of the present sequence are claimed. Zalphall
CC is expressed in lymph node, peripheral blood leucocytes, spleen and
CC thymus. The mRNA is also abundant in the Raji cell line (ATCC CCL 86)
CC derived from Burkitt's lymphoma. Zalphall polypeptides, and fusion
CC proteins, including chem, can be obtained by expression in recombinant
CC host cells. They are used: to detect ligands (also ligand agonists and
CC antagonists) that stimulate proliferation and/or development of
CC haematopoietic, lymphoid and myeloid cells; in vitro or in vivo, e.g. as
CC a replacement for serum in culture media; in soluble form to block ligand
CC activity (direct antagonists) and to detect ligand-expressing cancers; to
CC raise specific antibodies; and for purification of cognate ligands.
CC Agonistic ligands may stimulate cell-mediated immunity, e.g. for treating
CC (viral) infections associated with immunosuppression, improving the
CC activity of vaccines, suppressing tumours, treating leukaemia and
CC improving T-cell regeneration after bone marrow transplant. Antagonists
CC are useful as immunosuppressants, e.g. in the treatment of autoimmune
CC disease (e.g. rheumatoid arthritis, multiple sclerosis, diabetes), to
CC prevent transplant rejection and to treat T-cell leukemia or lymphoma
XX

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 7, 5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MPRGMAAPLLLLLLGSGMCPDLVCYDYDQYICILEMMNLHPSTLTLMQOYBELKD 60
Db 1 MPRGMAAPLLLLLLGSGMCPDLVCYDYDQYICILEMMNLHPSTLTLMQOYBELKD 60
Qy 61 EATSCSLHRSAHNATHATYTCHMDVFFHMADDFSVNITDQSGNYSGECCSFLAESTIKP 120
Db 61 EATSCSLHRSAHNATHATYTCHMDVFFHMADDFSVNITDQSGNYSGECCSFLAESTIKP 120
Qy 121 APPFNVTVTSSGQYNIWSRSDYEDPAFYMLKGKLYELOYRNKGDPMVAVSPRKRLISVDS 180
Db 121 APPFNVTVTSSGQYNIWSRSDYEDPAFYMLKGKLYELOYRNKGDPMVAVSPRKRLISVDS 180
Qy 181 RSVSLPLEFRKSSYELQVRAGPMPGSSYGQTSWSDPVIPTQOSEBELKEGMNPHLL 240
Db 181 RSVSLPLEFRKSSYELQVRAGPMPGSSYGQTSWSDPVIPTQOSEBELKEGMNPHLL 240
Qy 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWAVPSPERFPMPLKKGSGDFKKVAVGAPFTGSS 300
Db 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWAVPSPERFPMPLKKGSGDFKKVAVGAPFTGSS 300

```

QY 301 LELGPMSPREVSTLEVYSCHPPRSPAKRLQTLQELQPAELVESDGVKPSFTPTAQNSSG 360
DB 301 LELGPMSPREVSTLEVYSCHPPRSPAKRLQTLQELQPAELVESDGVKPSFTPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIIDVTYVLDAGPCTWPCSCEDDGYPALDDAGLEPSPGLEPDL 420
DB 361 SAYSEERDRPYGLVSIIDVTYVLDAGPCTWPCSCEDDGYPALDDAGLEPSPGLEPDL 420
QY 421 AGTTLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPWGGRSPGVSESEAGS 480
DB 421 AGTTLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPWGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVYIPPLSSPGQAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVYIPPLSSPGQAS 538

RESULT 6
AAB48001 standard; protein; 538 AA.
AAB48001;
AAB48001;
19-MAR-2001 (first entry)
Human IL-9/IL-2 receptor-like 16445 protein.
Interleukin-9; IL-9; IL-2 receptor; 16445 protein; inflammatory;
T-lymphocyte-related disorder; antiarthritic; antipsoriatic; human;
immunosuppressive; antidiabetic; antiallergic; antithyroid; cytostatic;
antidiarrhetic; nephrotropic; gene therapy.
Homo sapiens.
OS
XX
FH Key location/Qualifiers
FT Peptide 1..19
FT /note= "signal peptide"
FT Protein 20..538
FT /note= "mature protein"

W0200069880-A1.
23-NOV-2000.
18-MAY-2000; 2000MO-US013687.
PF 18-MAY-1999; 99US-00313913.
PR 18-MAY-1999; 99US-00313913.
PA (MILL-) MILLENNIUM PHARM INC.
PI Hodge MR;
XX WPI: 2001-016209/02.
DR N-PSDB; AAC84147.
XX
PT Novel interleukin-9/interleukin-2 receptor-like polypeptides useful for
PT diagnosis and treatment immune, inflammatory and respiratory disorders
PT and in screening assays for identifying modulators.
XX
PS Claim 8; Page 104-106; 119pp; English.

The invention relates to isolated human and murine interleukin-9 (IL-9)
/IL-2 receptor-like polypeptides. The plasmid containing the encoding
cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like
polypeptides (16445 proteins) can be recombinantly produced using
standard recombinant methodology. The 16445 proteins are used for
identifying their modulators and for diagnosis and treatment of immune,
inflammatory and respiratory disorders and disorders associated with
lungs, colon, kidney and lymphoid tissues including tonsil and thymus, in
particular T-lymphocyte-related disorders including atopic conditions
such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic
inflammatory diseases and graft versus host disease, disorders involving

CC the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney
CC disorders including polyarthritis kidney disease, cystic renal dysplasia,
CC disorders of the thymus including lymphomas, Hodgkin disease and
CC carcinoids. The 16445 polypeptides are also useful as modulating agents
CC in cellular processes including growth promoting activity, particularly
CC the antigen-independent proliferation of T-helper cell clones. The
CC encoding nucleic acid is useful as primers or hybridization probes for
CC the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for
CC tissue typing and in forensic biology. The present sequence represents
CC the human IL-9/IL-2 receptor-like polypeptide (AAH16445)
XX
SQ Sequence 538 AA;
Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 7, 5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRGMAAPLLILLQGGMGCPDLVCYTDYQTVLCILEMNNLHPSSTLTLTWQDYEELKD 60
DB 1 MPRGMAAPLLILLQGGMGCPDLVCYTDYQTVLCILEMNNLHPSSTLTLTWQDYEELKD 60
QY 61 EATSCSLHRSANATHTATYTCMDVFFHMDADIFSVNITDQSGNYSOECGFFLAESIKP 120
DB 61 EATSCSLHRSANATHTATYTCMDVFFHMDADIFSVNITDQSGNYSOECGFFLAESIKP 120
QY 121 APPPNVTVTFSGQYINISWRSDYEDPAFYMLKGLQYELQYRNKDDPMNVSRRKLISVDS 180
DB 121 APPPNVTVTFSGQYINISWRSDYEDPAFYMLKGLQYELQYRNKDDPMNVSRRKLISVDS 180
QY 181 RSVSLLELPFKDSYELQYRAGPMPSYOGTSEMSDPIYFOTOSBELKEGNNPHLL 240
DB 181 RSVSLLELPFKDSYELQYRAGPMPSYOGTSEMSDPIYFOTOSBELKEGNNPHLL 240
QY 241 LLLIVIFIPAFMSLKTHTPLMRKTIWAVSPERFPMPLKYGSGDFKKVGAAPFTGSS 300
DB 241 LLLIVIFIPAFMSLKTHTPLMRKTIWAVSPERFPMPLKYGSGDFKKVGAAPFTGSS 300
QY 301 LELGPMSPREVSTLEVYSCHPPRSPAKRLQTLQELQPAELVESDGVKPSFTPTAQNSSG 360
DB 301 LELGPMSPREVSTLEVYSCHPPRSPAKRLQTLQELQPAELVESDGVKPSFTPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIIDVTYVLDAGPCTWPCSCEDDGYPALDDAGLEPSPGLEPDL 420
DB 361 SAYSEERDRPYGLVSIIDVTYVLDAGPCTWPCSCEDDGYPALDDAGLEPSPGLEPDL 420
QY 421 AGTTLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPWGGRSPGVSESEAGS 480
DB 421 AGTTLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPWGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVYIPPLSSPGQAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVYIPPLSSPGQAS 538

RESULT 7
AAB81960 standard; protein; 538 AA.
AAB81960;
AAB81960;
25-NOV-2002 (first entry)
Human 16445 protein.
Interleukin; IL-9; IL-2; 16445; antidiabetic; antiallergic; human;
antiinflammatory; antipsoriatic; immunosuppressive; cytostatic; virucide;
antirheumatic; antidiarrhetic; antidiabetic; antithyroid; dermatologic;
nephrotropic; antibacterial; tuberculostatic; antileprotic; antipyretic;
antitumor; gene therapy; receptor.
Homo sapiens.
OS
XX
FN US2002090680-A1.

XX	PD		11-JUL-2002.
XX	PF	26-SEP-2001; 2001US-00965313.	
XX	PR	18-MAY-1999; 99US-00313913.	
XX	PR	18-MAY-2000; 2000US-00574100.	
XX	PA	(MILL-) MILLENNIUM PHARM INC.	
XX	PI	Hodge MR;	
XX	DR	WPI; 2002-655832/70.	
XX	DR	N-PBDB; ABQ79536.	
PT	PT	New interleukin-9/interleukin-2 receptor-like polypeptides and polynucleotides for diagnosing, treating respiratory, T-lymphocyte related disorders and disorders associated with lung, colon, kidney and lymphoid tissues.	
PS	PT	Claim 8; Page 31-33; 54pp; English.	
XX	CC	The invention relates to isolated interleukin (IL)-9/IL-2 receptor-like polypeptide, 16445. The 16445 polypeptide can be expressed by standard recombinant methodology. The 16445 polypeptide, polynucleotides and their modulators are useful for modulating the immune, inflammatory and respiratory responses, for the diagnosis and treatment of immune and respiratory disorders, particularly for the treatment and diagnosis of T- lymphocyte-related disorders, including, atopic conditions, such as asthma and allergy, including allergic rhinitis, psoriasis, the effects of pathogen infection, chronic inflammatory diseases, organ-specific autoimmunity, graft rejection, and graft versus host disease. The molecules are also useful as modulating agents in a variety of cellular processes including growth promoting activity, particularly the antigen independent proliferation of T helper cell clones, and direct effects on normal haemopoietic progenitors, human T cells, B cells, thymocytes, thymic lymphomas and neuronal cell lines. They are useful for the modulation, diagnosis, and treatment of immune, inflammatory, and respiratory disorders and disorders associated with lungs, colon, kidney, and lymphoid tissues including tonsil and thymus. The present sequence represents a human 16445 polypeptide	
XX	SQ	Sequence 538 AA;	
Query Match		100.0%; Score 2958; DB 5; Length 538;	
Best Local Similarity		100.0%; Pred. No. 7, 5e-240;	
Matches 538; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;	
OY	1	MPRGNAAPDLLLLLOGGWCPCDVLVCTDYLTQTICILEMMNLHSPSTLTLTWODYYEELKD	60
Db	1	MPRGMAAPDLLLLLOGGWCGCPDLVCYTDTYLQVICILEMMNLHPSTLTLTWODYYEELKD	60
OY	61	EATSGSLRSANAHATTYTCMDVFHFMAADIFESVNITTDOSGNVSOGCSFTLAESTKP	120
Db	61	EATSGSLRSANAHATTYTCMDVFHFMAADIFSVNITTDOSGNVSOGCSFTLAESTKP	120
OY	121	APPFNVITYTFSGGYNISMSRSDYEDPAFWMLKKGLOLEYLOYRNRRGPPMAVSPRKLIISYS	180
Db	121	APPFNVITYTFSGGYNISMSRSDYEDPAFWMLKKGLOLEYLOYRNRRGPPMAVSPRKLIISYS	180
OY	181	RSVSLILPLEFRKDSYELQVRAGPMPGSSYGCTSWSEWSDPVIFTQOSEELKEGMNPHLL	240
Db	181	RSVSLILPLEFRKDSYELQVRAGPMPGSSYGCTSWSEWSDPVIFTQOSEELKEGMNPHLL	240
OY	241	LLLIVTVITPAWLSUKTHPLWLAKKIIVAVPEPEFPFLPYXGCGDFRTKWVGAFPTSSS	300
Db	241	LLLIVTVITPAWLSUKTHPLWLAKKIIVAVPEPEFPFLPYXGCGDFRTKWVGAFPTSSS	300
OY	301	LELGWSPDEVPTLEVSGCHPPRPSPAKRLQLTELQEPALVESDGVKPRSFWPTAONSGG	360
Db	301	LELGWSPDEVPTLEVSGCHPPRPSPAKRLQLTELQEPALVESDGVKPRSFWPTAONSGG	360
OY	361	SAYSEERRPYGLVVIDVTYVDAGEGCTWPSCSDDGYPALDLDAIGLEPSFGLEDPLLD	420

Dd			361 SAYSERDRPRYGLVSDIDVTYVDAGPCITWPCSCEDDGCPALDLDNGLSPSLDEPLUD	420
Oy		421 AGTVLSCGCVSACSGPGLGGPIGLSLLDLKLPPLADGEDMAGLI PMCGRS PGVSBSEAGS	480	
Dd		421 AGTIVLSGCVCVASGPGLGGPIGLSLLDLRKLPPLAGEDWAGLI PMCGRRPGCVSESEAGS	480	
Oy		481 PLAGIDMTDFDSGFVFQSSPVFCDFTSRPDGEPRSTRVMVVTPPLSSSPGPAS	538	
Dd		481 PLAGIDMTDFDSGFVFQSSPVFCDFTSRPDGEPRSTRVMVVTPPLSSSPGPAS	538	
 RESULT 8 AAU11912				
ID	AAU11912 standard; protein; 538 AA.			
XX	AAU11912;			
DT	09-APR-2002 (first entry)			
XX				
XX				
De	Human MU-1 haematopoietin receptor superfamily chain protein sequence.			
Kw	Human; MU-1; haematopoietin receptor superfamily chain; thyroiditis;			
Km	immune deficiency; anaemia; autoimmune disorder; multiple sclerosis;			
Kw	systemic lupus erythematosus; rheumatoid arthritis;			
Kw	pulmonary inflammation; insulin dependent diabetes mellitus;			
XX	nutritional supplement; cytokine receptor family.			
OS	Homo sapiens.			
XX				
FH	Key Location/Qualifiers			
FT	Domain 237..254 /note= "Transmembrane domain"			
Pt				
PN	WO200185792-A2.			
PD				
PF	15-NOV-2001.			
XX				
XX	11-MAY-2001; 2001WO-USO15395.			
XX				
Pr	05-NOV-1999; 99US-00569384.			
PA	(GENY) GENETICS INST INC.			
PI				
Dr	Donaldson DD, Unger MJ, Young DA, Wlitters MJ, Lowe L, Collins M;			
Bx	N-PsDB; MAS17248.			
PT	New polypeptide, useful for identifying compounds binding to MU-1, and			
PT	for treating multiple sclerosis, rheumatoid arthritis, diabetes and			
PT	asthma, comprises the isolated murine MU-1 protein, and a hematopoietin			
XX	receptor superfamily chain.			
PS				
XX	Disclosure; Fig 4; 59pp; English.			
CC	The present invention relates to a new murine MU-1 protein, a			
CC	haematopoietin receptor superfamily chain, comprising a fully defined			
CC	sequence of 529 amino acids (AAU11915) as given in the specifications or			
CC	fragment of protein having MU-1 biological activity. The molecules of the			
CC	invention may exhibit cytokine, cell proliferation or cell			
CC	differentiation activity and may also exhibit immune stimulating or			
CC	immune suppressing activity and can be useful in the treatment of various			
CC	immune deficiencies and disorders including severe combined			
CC	immunodeficiency (SCID). Another use of the invention is treating			
CC	autoimmune disorders such as connective tissue disease, multiple			
CC	sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune			
CC	pulmonary inflammation, autoimmune thyroiditis, insulin dependent			
CC	diabetes mellitus, and autoimmune inflammatory eye disease. The invention			
CC	is useful for the treatment of myeloid or lymphoid cell deficiencies and			
CC	in treating various anaemias or for use in conjunction with			
CC	irradiation/chemotherapy to stimulate the production of erythroid			
CC	precursors and/or erythroid cells. The polynucleotides and proteins can			

CC also be used as nutritional sources or supplements. The present protein sequence represents the human MU-1 haemopoietin receptor superfamily chain. MU-1 is also a member of the cytokine receptor family. This CC sequence was used in the invention for the characterisation of previously unknown members of the haemopoietin receptor superfamily

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 5; Length 538;

Best Local Similarity 100.0%; Pred. No. 7.5e-240; Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYLCYIEMNNLHPSTLTTLTWQDQYBELKD 60
DB 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYLCYIEMNNLHPSTLTTLTWQDQYBELKD 60
QY 61 EATSCSLHRSANAHNAHTATYTCMDVFFHMDIFSVNITDQSGYSGECGFFLAESIKP 120
DB 61 EATSCSLHRSANAHNAHTATYTCMDVFFHMDIFSVNITDQSGYSGECGFFLAESIKP 120
QY 121 APPENVTVTFSGQYINISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSPRRKLISVDS 180
DB 121 APPENVTVTFSGQYINISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSPRRKLISVDS 180
QY 181 RSVSLPLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPYIFQTQSEELKEGNNPHLL 240
DB 181 RSVSLPLEFRKDSYELQYRAGMPGSSYQGTWSEMSDPYIFQTQSEELKEGNNPHLL 240
QY 241 LLLLVIFIPAFWMLKTHPLWRLMKKIWAVPSPERFMPFLKGGSGDPKKVAGAPFTGSS 300
DB 241 LLLLVIFIPAFWMLKTHPLWRLMKKIWAVPSPERFMPFLKGGSGDPKKVAGAPFTGSS 300
QY 301 LELGPMSPPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFWPTAONSGG 360
DB 301 LELGPMSPPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFWPTAONSGG 360
QY 361 SANSEEDRPYGLVSTITVYLDAGRCTWPCSCEDDGYPLDDAGLEPFGLEDPLD 420
DB 361 SANSEEDRPYGLVSTITVYLDAGRCTWPCSCEDDGYPLDDAGLEPFGLEDPLD 420
QY 421 AGTTVLSCGCVSAGSPGLGPGISLDRKPLPLADGEDMAGCLPMGGSPGCVSESEAGS 480
DB 421 AGTTVLSCGCVSAGSPGLGPGISLDRKPLPLADGEDMAGCLPMGGSPGCVSESEAGS 480
QY 481 PLAGLMDTDPDGSFVGSPPVSCDFTSPGDEGPPRSYLRQWVVIIPPLSSPPGQAS 538
DB 481 PLAGLMDTDPDGSFVGSPPVSCDFTSPGDEGPPRSYLRQWVVIIPPLSSPPGQAS 538

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RESULT 9

AAE13726 ID AAE13726 standard; protein; 538 AA.

XX AAE13726;

XX 26-FEB-2002 (first entry)

XX Human soluble zalphal1 cytokine receptor protein.

XX Human; zalphal1; cytokine receptor; immunosuppressive; cytostatic;
 KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;
 KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;
 KW viral infection.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Protein 20..538 /label= Signal_peptide

FT Protein 20..538 /label= Mature_zalphal1_protein

```

FT Domain 20..237
FT /label= Cytokine_binding_domain
FT Domain 120..123
FT /label= Domain_linker
FT Region 192..202
FT /note= "Penultimate strand region"
FT Domain 214..218
FT /note= "MSXMS motif"
FT Domain 238..255
FT /label= Transmembrane_domain
FT Domain 256..538
FT /label= Intracellular_signalling_domain
FT Region 267..273
FT /note= "Box I signalling site"
FT Region 301..304
FT /note= "Box II signalling site"
FT Binding-site 519..522
FT /label= STAT3_binding_site

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XX W0200177171-A2.

XX 18-OCT-2001.

XX 03-APR-2001; 2001WO-US010872.

XX 05-APR-2000; 2000US-0194731P.

XX 28-JUL-2000; 2000US-0222121P.

XX (ZYMO) ZYMOGENETICS INC.

PI Sprechter CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ,

XX WPI; 2002-025898/03.

XX N-PSDB; AAD22918.

PT Novel soluble receptor polypeptides and polynucleotides used as cytokine

PT antagonist for stimulating ligand activity-induced proliferation of

PT hematopoietic cells and for suppressing immune response in a mammal.

PS Example 1; Page 172-173; 243pp; English.

XX The invention relates to an isolated soluble zalphal1 cytokine receptor polypeptide and their cDNA molecules. Zalphal1 proteins are useful for inhibiting or antagonising the ligand activity-induced proliferation of haematopoietic cells and haematopoietic cell progenitors preferably CC lymphoid cells which are natural killer cells or cytotoxic T cells. CC Zalphal1 is useful for treating immune and inflammatory disorders, for CC reducing proliferation of neoplastic B or T cells, for suppressing an CC immune response in a mammal exposed to an antigen or pathogen. Zalphal1 CC is useful for treating diseases that require immune regulation including CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes; CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease, CC sepsis, viral infection (dengue virus infection) and cancer. The present CC sequence is human soluble zalphal1 cytokine receptor protein

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 5; Length 538;

Best Local Similarity 100.0%; Pred. No. 7.5e-240; Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYLCYIEMNNLHPSTLTTLTWQDQYBELKD 60
DB 1 MPRGMAAPLLLLLLQGGMGCPDLYCYTDYLCYIEMNNLHPSTLTTLTWQDQYBELKD 60
QY 61 EATSCSLHRSANAHNAHTATYTCMDVFFHMDIFSVNITDQSGYSGECGFFLAESIKP 120
DB 61 EATSCSLHRSANAHNAHTATYTCMDVFFHMDIFSVNITDQSGYSGECGFFLAESIKP 120
QY 121 APPENVTVTFSGQYINISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSPRRKLISVDS 180
DB 121 APPENVTVTFSGQYINISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSPRRKLISVDS 180

```

```
QY 181 RSVSLPLPERFRKSSYELQVRAGPMGSSSYQGTWSEMSDPVIFOTOSBELKEGNPHLL 240
DB 181 RSVSLPLPERFRKSSYELQVRAGPMGSSSYQGTWSEMSDPVIFOTOSBELKEGNPHLL 240
QY 241 LLLLVIFIFAFWMLKTHPLMLMKKIWA VSPERFEMPLYKCGSGDFKKWVGAPFTGSS 300
DB 241 LLLLVIFIFAFWMLKTHPLMLMKKIWA VSPERFEMPLYKCGSGDFKKWVGAPFTGSS 300
QY 301 LEIGPMSPEVPSTLEVYSCHPFRSPAKRLQLTLEQPAELVESDGVKPFSPFTAONSGG 360
DB 301 LEIGPMSPEVPSTLEVYSCHPFRSPAKRLQLTLEQPAELVESDGVKPFSPFTAONSGG 360
QY 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPGLJEDPLD 420
DB 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPGLJEDPLD 420
QY 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKRPPLADGEDMAGCLPMGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKRPPLADGEDMAGCLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTFDSDGVSDCSSPVECDFTSPGDEGPPRSYLKQWVVI PPLSSPGPOAS 538
DB 481 PLAGLMDTFDSDGVSDCSSPVECDFTSPGDEGPPRSYLKQWVVI PPLSSPGPOAS 538

RESULT 10
AAU11978
ID AAU11978 standard; protein; 538 AA.
XX
AC AAU11978;
XX
DT 09-APR-2002 (first entry)
XX
XX Human zai1phail receptor polypeptide.
DE
XX
XX Cytokine; zai1phail ligand; zai1phail receptor; NK cell progenitor;
KM natural killer cell proliferation; T-cell proliferation;
KM B-cell proliferation; anti-tumour response; immune system;
KW immunostimulant; cytoelastic; human.
OS
XX
XX Homo sapiens.
XX
XX US6307024-B1.
XX
XX 23-OCT-2001.
XX
XX 09-MAR-2000; 2000US-00522217.
XX
XX 09-MAR-1999; 99US-0123547P.
XX
XX 11-MAR-1999; 99US-0123904P.
XX
XX 01-JUL-1999; 99US-0142013P.
XX
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX
XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI; 2002-040208/05.
XX
XX N-PSDB; AAS20642.
XX
XX
XX New zai1phail ligand polypeptides and polynucleotides, useful for
XX
XX stimulating proliferation, activation, differentiation and/or induction
XX
XX of inhibition of specialized cell function, or for stimulating an
XX
XX antigenic response.
XX
XX
XX Claim 1; Col 191-194; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
XX
XX zai1phail ligand and the polynucleotide encoding it. The invention also
XX
XX gives the sequence for the zai1phail receptor and the polynucleotide
XX
XX encoding it. The zai1phail ligand polypeptide stimulates proliferation of
XX
XX natural killer (NK) cells or NK cell progenitors, the activation of NK
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CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
CC zai1phail ligand polypeptide is also useful in preparing antibodies that
CC bind to zai1phail ligand epitopes. The zai1phail ligand polynucleotides can
CC be used as probes or primers to clone regions of a zai1phail ligand gene,
CC and in gene therapy. Zai1phail ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC human zai1phail receptor polypeptide
XX
XX
XX Sequence 538 AA:
XX
XX
XX Query Match 100.0%; Score 2958; DB 5; Length 538;
XX
XX Best Local Similarity 100.0%; Pred. No.7,5e-240;
XX
XX Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MPRGMAAPLLLLLOGMGCPDLVCTDYLTQVTCILEMNNLHPSTLTWTWQDYEBLKD 60
DB 1 MPRGMAAPLLLLLLLOGMGCPDLVCTDYLTQVTCILEMNNLHPSTLTWTWQDYEBLKD 60
QY 61 EATSCSIHRSANAHATATYTCHEMDVFHFMADDIFS VNITDQSGNYGECGSLAASIKP 120
DB 61 EATSCSIHRSANAHATATYTCHEMDVFHFMADDIFS VNITDQSGNYGECGSLAASIKP 120
QY 121 APPENVTVTFSSGOVNI SWRSDYEDPAFYMLKGLQYELQVRNKGDDPMAVSPRKLISVDS 180
DB 121 APPENVTVTFSSGOVNI SWRSDYEDPAFYMLKGLQYELQVRNKGDDPMAVSPRKLISVDS 180
QY 181 RSVSLPLPERFRKSSYELQVRAGPMGSSSYQGTWSEMSDPVIFOTOSBELKEGNPHLL 240
DB 181 RSVSLPLPERFRKSSYELQVRAGPMGSSSYQGTWSEMSDPVIFOTOSBELKEGNPHLL 240
QY 241 LLLLVIFIFAFWMLKTHPLMLMKKIWA VSPERFEMPLYKCGSGDFKKWVGAPFTGSS 300
DB 241 LLLLVIFIFAFWMLKTHPLMLMKKIWA VSPERFEMPLYKCGSGDFKKWVGAPFTGSS 300
QY 301 LEIGPMSPEVPSTLEVYSCHPFRSPAKRLQLTLEQPAELVESDGVKPFSPFTAONSGG 360
DB 301 LEIGPMSPEVPSTLEVYSCHPFRSPAKRLQLTLEQPAELVESDGVKPFSPFTAONSGG 360
QY 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPGLJEDPLD 420
DB 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYPALDLDALEBPGLJEDPLD 420
QY 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKRPPLADGEDMAGCLPMGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGPGSLDLRLKRPPLADGEDMAGCLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTFDSDGVSDCSSPVECDFTSPGDEGPPRSYLKQWVVI PPLSSPGPOAS 538
DB 481 PLAGLMDTFDSDGVSDCSSPVECDFTSPGDEGPPRSYLKQWVVI PPLSSPGPOAS 538

RESULT 11
ABR61402
ID ABR61402 standard; protein; 538 AA.
XX
XX
XX ABR61402;
XX
XX
XX 12-AUG-2003 (first entry)
XX
XX
XX Human IL-21R SEQ ID NO:2.
XX
XX
XX arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;
XX
XX immune cell activity; cancer; infectious disorder; antiheumatic;
XX
XX antiarthritic; osteopathic; antipsoriatic; cytosarctic; antibacterial;
XX
XX virucide; antiparasitic; immunosuppressive; antidiabetic; dermatologic;
XX
XX neuroprotective; anticancer; antiallergic; antianemic; hepatotropic;
XX
XX antithyroid; antiinflammatory; immune response; immune disorder;
XX
XX autoimmune disease; human.
XX
```

OS Homo sapiens.
 XX W02003028630-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 04-OCT-2002; 2002WO-US029839.
 XX
 PR 04-OCT-2001; 2001US-00972218.
 PR 17-APR-2002; 2002US-0373746P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Carter L, Whitters MJ, Collins M, Young DA, Larsen G,
 PI Donaldson DD, Lowe LD, Dunnesi K, Ma M, Witek JS, Kasanian MT,
 PI Ungar M.
 XX
 XX WPI: 2003-430146/40.
 DR N-PSDB; ACC80861.
 XX
 PT Treating or preventing arthritic disorder, cancer or infectious disorders
 PT in a subject, involves administering a modulator of interleukin-21 or its
 PT receptor which modulate immune cell activity.
 XX
 PS Claim 40; Fig 28; 176pp; English.
 XX
 CC The invention relates to a novel method for treating or preventing an
 CC arthritic disorder in a subject. The method involves administering to the
 CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist
 CC optionally in combination with another therapeutic agent, to inhibit or
 CC reduce immune cell activity in the subject. The method is also useful for
 CC treating or preventing cancer or an infectious disorder, in a subject, by
 CC administering IL-21/IL-21R agonist, to increase immune cell activity. The
 CC method of the invention has antirheumatic, antiarthritic, osteopathic,
 CC antiporiatic, cytostatic, antibacterial, virucide, antiparasitic,
 CC immunosuppressive, antidiabetic, neuroprotective, dermatological,
 CC anticancer, antistimatic, antiallergic, antianemic, hepatocytic,
 CC antitumor, and antiinflammatory activity. The method is useful for
 CC treating or preventing an arthritic disorder such as rheumatoid
 CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic
 CC arthritis or ankylosing spondylitis, and also cancer such as solid
 CC tumour, soft tissue tumour or metastatic lesion, or an infectious
 CC disorder such as bacterial, viral or parasitic infection in a mammal,
 CC preferably human. A method of the invention is also useful for
 CC increasing the ability of a vaccine composition containing an antigen to
 CC elicit a protective immune response in a subject against the antigen.
 CC The antigen is from a pathogen such as virus, bacterium or protozoan, or
 CC from cancer or tumour cell antigen, or expressed on the surface of cancer
 CC cell. An alternative method of the invention is useful for modulating the
 CC activity of immune or haematopoietic cells and thus to treat or prevent a
 CC variety of immune disorders, such as autoimmune diseases, for example
 CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus
 CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,
 CC hepatitis, Graves's disease, graft versus host disease, and scleroderma.
 CC The present sequence is used in an exemplification of the invention
 XX
 SQ Sequence 538 AA;
 Query Match 100.0%; Score 2958; DB 6; Length 538;
 Best Local Similarity 100.0%; Pred. No. 7.5e-240;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 RSVSLLPLERKDSVYELQVRAGMPGSSYQGTWSESDPVITPOTQSEELKEGNPHLL 240
 D 181 RSVSLLPLERKDSVYELQVRAGMPGSSYQGTWSESDPVITPOTQSEELKEGNPHLL 240
 QY 241 LLLLVIVIFPAFWSLKTPLMLRLMKKIWAVPSEDFPMPYKGCSDPKKVGAPFTGSS 300
 DB 241 LLLLVIVIFPAFWSLKTPLMLRLMKKIWAVPSEDFPMPYKGCSDPKKVGAPFTGSS 300
 QY 301 LEIGPMSPEVPSTLEVYSCHPPPSPAKRLQTLTQEPALVESDGVKPSFMPAQNSSG 360
 DB 301 LEIGPMSPEVPSTLEVYSCHPPPSPAKRLQTLTQEPALVESDGVKPSFMPAQNSSG 360
 QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTPCSCEDDGYPALDLDALESPGLJEDPLD 420
 DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTPCSCEDDGYPALDLDALESPGLJEDPLD 420
 QY 421 AGTTVLSGCVSAGSPGLGPGLSLDRLRPLADGEDMAGGLPMGGRSPGVSESEAGS 480
 DB 421 AGTTVLSGCVSAGSPGLGPGLSLDRLRPLADGEDMAGGLPMGGRSPGVSESEAGS 480
 QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPQDEGPPSYLRQWVVIIPPLSSPGPOAS 538
 DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPQDEGPPSYLRQWVVIIPPLSSPGPOAS 538
 RESULT 12
 AAEL1939
 ID AAEL1939 standard; protein; 538 AA.
 XX
 AC AAEL1939;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human interleukin-21 (IL-21) receptor.
 XX
 KW Interleukin-21; antagonist; cancer; inflammatory; autoimmune disorder;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW myasthenia gravis; diabetes; human; zaiaphall receptor; IL-21 receptor.
 OS
 XX Homo sapiens.
 XX
 PN W02003040313-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 28-OCT-2002; 2002WO-US034502.
 XX
 PR 05-NOV-2001; 2001US-0337586P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, West JW, Novak JE;
 PI WPI: 2003-441547/41.
 DR N-PSDB; AAD47859.
 XX
 PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
 PT and treating disorders with aberrant expression or activity of the IL-21
 PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
 PT diabetes.
 XX
 PS Example 1; Page 65-67; 71pp; English.
 XX
 CC The invention relates to polynucleotides and polypeptides of interleukin-
 CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
 CC that is not detectable in receptor binding studies. The antagonists of
 CC the invention have mutations in the D helix of the IL-21 molecule, and
 CC can be used to inhibit the activity of IL-21 with its cognate receptor.
 CC The IL-21 antagonists are useful for diagnosing and treating disorders
 CC involving the aberrant expression or activity of the IL-21 polypeptide,
 CC such as cancer, inflammatory and autoimmune disorders, including
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,

CC myasthenia gravis and diabetes. The polypeptides can also be used to
CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides.
CC and for enhancing in vivo killing of target tissues. The present sequence
CC is human IL-21 receptor (originally designated zalphail receptor)
XX
SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYIQTYICILEMNNLHPSTLTTLTWODQYELKD 60
DB 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYIQTYICILEMNNLHPSTLTTLTWODQYELKD 60
QY 61 EATSCSLHRSANAHNATHTYTCMDVFFHMAADDIFSUNITDQSGNYSOEGCSFLAESIKP 120
DB 61 EATSCSLHRSANAHNATHTYTCMDVFFHMAADDIFSUNITDQSGNYSOEGCSFLAESIKP 120
QY 121 APPENVTVTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMAVSPRRKLISVDS 180
DB 121 APPENVTVTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMAVSPRRKLISVDS 180
QY 181 RSVSLPLEFRKDSYELQYRAGPMGSSYOGTSEMSDPVIFOTQSEELKEGNNPHLL 240
DB 181 RSVSLPLEFRKDSYELQYRAGPMGSSYOGTSEMSDPVIFOTQSEELKEGNNPHLL 240
QY 241 LLLLVIVIFAPFWSLKTNPRLMKKIWAIVSPERFPMPLKYGSGDFKKNVGAAPFTGSS 300
DB 241 LLLLVIVIFAPFWSLKTNPRLMKKIWAIVSPERFPMPLKYGSGDFKKNVGAAPFTGSS 300
QY 301 LELGPMSPVEPSTLEVYSCHPSPSPAKRLQTLTEQEPALVESGVPKSPPTAQNSSGG 360
DB 301 LELGPMSPVEPSTLEVYSCHPSPSPAKRLQTLTEQEPALVESGVPKSPPTAQNSSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
QY 421 AGTTVSLCGCVSAGSPGLGPGLSLLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTVSLCGCVSAGSPGLGPGLSLLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPLSSPGQAS 538
DB 481 PLAGLMDTDFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPLSSPGQAS 538

RESULT 13
ABU62888
ID ABU62888 standard; proteoin; 538 AA.

XX AC ABU62888;
XX DT 15-SEP-2003 (first entry)
XX DE Human MU-1 haematopoietic receptor superfamily chain.
XX KM Human; MU-1; haematopoietic receptor superfamily chain; immunomodulator;
XX KM cytoactive; antibacterial; virucide; antianaemic; gene therapy;
XX KM haematopoiesis; anaemias; immune response; cancer; infection;
XX KM transplanted organ; cytokine; receptor.
XX OS Homo sapiens.
XX PN US2003049798-A1.
XX PD 13-MAR-2003.
XX PF 04-OCT-2001; 2001US-00972218.
XX PR 17-MAR-1998; 98US-00040005.
XX PR 26-APR-2000; 2000US-00560766.

PR 11-MAY-2000; 2000US-00569384.

XX (CART/) CARTER L.
PA (WHIT/) WHITTERS M J.
PA (COLL/) COLLINS M.
PA (YOUN/) YOUNG D A.
PA (DONA/) DONALDSON D D.
PA (LOWE/) LOWE L D.
PA (UNGE/) UNGER M.
XX Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;
PI Lowe LD, Unger M;
XX WPI: 2003-512354/48.
DR N-PSDB: ACD26717.

XX New fusion polypeptide for regulating hematopoiesis and immune responses,
PT comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion
PT polypeptide.

XX Claim 13; Fig 4; 26pp; English.

XX The invention describes a fusion polypeptide comprising at least a
CC fragment of a MU-1 polypeptide and a non-MU-1 fusion polypeptide. The
CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of
CC anaemias) and/or immune responses (e.g. immune response to cancer,
CC infections or to a transplanted organ) and in identifying other members
CC of the haematopoietic superfamily, including cytokines and receptors. The
CC polynucleotide may be used to express recombinant protein for analysis,
CC characterisation or therapeutic use; and as markers for tissues or
CC chromosomes. The polypeptide and polynucleotide may also be used as
CC nutritional sources or supplements. This is the amino acid sequence of
CC human MU-1 haematopoietic receptor superfamily chain

XX Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 7.5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYIQTYICILEMNNLHPSTLTTLTWODQYELKD 60
DB 1 MPRGMAAPLLLLLLQGGMGCPDLVCYTDYIQTYICILEMNNLHPSTLTTLTWODQYELKD 60
QY 61 EATSCSLHRSANAHNATHTYTCMDVFFHMAADDIFSUNITDQSGNYSOEGCSFLAESIKP 120
DB 61 EATSCSLHRSANAHNATHTYTCMDVFFHMAADDIFSUNITDQSGNYSOEGCSFLAESIKP 120
QY 121 APPENVTVTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMAVSPRRKLISVDS 180
DB 121 APPENVTVTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMAVSPRRKLISVDS 180
QY 181 RSVSLPLEFRKDSYELQYRAGPMGSSYOGTSEMSDPVIFOTQSEELKEGNNPHLL 240
DB 181 RSVSLPLEFRKDSYELQYRAGPMGSSYOGTSEMSDPVIFOTQSEELKEGNNPHLL 240
QY 241 LLLLVIVIFAPFWSLKTNPRLMKKIWAIVSPERFPMPLKYGSGDFKKNVGAAPFTGSS 300
DB 241 LLLLVIVIFAPFWSLKTNPRLMKKIWAIVSPERFPMPLKYGSGDFKKNVGAAPFTGSS 300
QY 301 LELGPMSPVEPSTLEVYSCHPSPSPAKRLQTLTEQEPALVESGVPKSPPTAQNSSGG 360
DB 301 LELGPMSPVEPSTLEVYSCHPSPSPAKRLQTLTEQEPALVESGVPKSPPTAQNSSGG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
QY 421 AGTTVSLCGCVSAGSPGLGPGLSLLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTVSLCGCVSAGSPGLGPGLSLLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFVSGDCSSPVECDFTSPGDEGPPRSYLQWVVIIPPLSSPGQAS 538

Db 481 PLAGLMDTDFDSGVGSDCSSPVECDFTSPGDEGPPRSYLQWVVIPEPLSSPGPOAS 538
RESULT 14
ABW00881
ID ABW00881 standard; protein; 538 AA.
AC ABW00881;
XX 15-JAN-2004 (first entry)
XX Human cytokine receptor, zalphall protein.
XX
XX Cytokine receptor; Zalphall; cell proliferation; cell development;
XX spleenic disorder; blood disorder; bone disorder; immune disorder;
XX haematopoietic; lymphoid; inflammatory; therapy; receptor; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT 20..538
FT Protein /note= "Mature human zalphall protein"
FT Binding-site 20..237
FT /note= "Cytokine-binding domain"
FT Region 120..123
FT /note= "Domain linker"
FT Region 192..202
FT /note= "Penultimate strand region"
FT Domain 214..218
FT /note= "WSXWS motif"
FT Domain 238..255
FT /note= "Transmembrane domain"
FT Domain 256..538
FT /note= "Intracellular signalling domain"
FT Region 267..273
FT /note= "Box I signalling site"
FT Region 301..304
FT /note= "Box II signalling site"
XX
XX US6576744-B1.
XX
XX 10-JUN-2003.
XX
XX 23-SEP-1999; 99US-00404641.
XX
XX 23-SEP-1998; 98US-0100896P.
XX 09-MAR-1999; 99US-0123546P.
XX 06-JUL-1999; 99US-0142574P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX
XX WPI; 2003-799829/75.
XX DR N-PSDB; AAD61882.
XX
XX Novel cytokine receptor zalphall useful for treating lymphoid, immune,
XX inflammatory, spleenic, blood or bone disorders.
XX
XX Claim 1; Fig 2; Opp; English.
XX
XX The invention relates to a cytokine receptor designated zalphall and its
XX nucleic acid sequence. Zalphall protein is useful for detecting ligands
XX that stimulate the proliferation and/or development of haematopoietic,
XX lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful
XX in identifying a region of the genome associated with human disease
XX states. Zalphall protein is useful for treating lymphoid, immune,
XX inflammatory, spleenic, blood or bone disorders. The present sequence is
XX human Zalphall protein

SO Sequence 538 AA;
Query Match 100.0%; Score 2958; DB 7; Length 538;
Best Local Similarity 100.0%; Pred. No. 7,5e-240;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRGMALPLLLLLQGGMGCPDLVCTDYDQTVICILEMNLHPSTLTLTQDDQYEEELKD 60
Db 1 MPRGMALPLLLLLQGGMGCPDLVCTDYDQTVICILEMNLHPSTLTLTQDDQYEEELKD 60
Qy 61 EATSCSLHRSANATHTATYTCMDVFHMAADIFSVNITDQSGVSOEGSFLAESIKP 120
Db 61 EATSCSLHRSANATHTATYTCMDVFHMAADIFSVNITDQSGVSOEGSFLAESIKP 120
Qy 121 APPNVTVTSSGQYNISWSDYEDPAFYMLKGLQYELQYRNKDDPMAVSPRRKLISVDS 180
Db 121 APPNVTVTSSGQYNISWSDYEDPAFYMLKGLQYELQYRNKDDPMAVSPRRKLISVDS 180
Qy 181 RSVSLPLEFRKDSYVLOVRAGMPGSSYOGTWSEMSDPVIFOTOSBELKEGNNPHLL 240
Db 181 RSVSLPLEFRKDSYVLOVRAGMPGSSYOGTWSEMSDPVIFOTOSBELKEGNNPHLL 240
Qy 241 LLLLVIFIPAFMSLKTHPMLRWLKKIWAAPSRRFFMPLYKSGSDFKKVGAFTGSS 300
Db 241 LLLLVIFIPAFMSLKTHPMLRWLKKIWAAPSRRFFMPLYKSGSDFKKVGAFTGSS 300
Qy 301 LEIGPMSPEVPSTLEVYSCHPSPSPAKRLQTLQEPALVESDGVKPKSPFWPTAONSGG 360
Db 301 LEIGPMSPEVPSTLEVYSCHPSPSPAKRLQTLQEPALVESDGVKPKSPFWPTAONSGG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLJEDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLJEDPLLD 420
Qy 421 AGTVLSCGCVSAGSPGLGSPGLSLDLRLKPLADGEMWAGGLPMGGRSPGVSESEAGS 480
Db 421 AGTVLSCGCVSAGSPGLGSPGLSLDLRLKPLADGEMWAGGLPMGGRSPGVSESEAGS 480
Qy 481 PLAGLMDTDFDSGVGSDCSSPVECDFTSPGDEGPPRSYLQWVVIPEPLSSPGPOAS 538
Db 481 PLAGLMDTDFDSGVGSDCSSPVECDFTSPGDEGPPRSYLQWVVIPEPLSSPGPOAS 538
RESULT 15
ADG87460
ID ADG87460 standard; protein; 538 AA.
XX
XX ADG87460;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human zalphall protein.
XX
XX zalphall; anaemia; human; gene therapy.
XX
XX Homo sapiens.
XX
XX
XX
XX Key Location/Qualifiers
FT Peptide 1..19
FT /label= Signal_peptide
FT 20..538
FT Protein /note= "Human mature zalphall protein"
FT Domain 20..237
FT /note= "Cytokine binding domain"
FT Region 120..123
FT /note= "Domain linker"
FT Region 192..202
FT /note= "Penultimate strand region"
FT Domain 238..255
FT /note= "Transmembrane domain"
FT Domain 256..538
FT /note= "Complete intracellular signalling domain"
FT Region 267..273

FT	Region
FT	/notes="Box I signaling site"
FT	301. .304
FT	/note="Box II signaling site"

PN US2003148447-A1.

PD 07-AUG-2003.

PF 13-SEP-2002; 2002US-00243072.

PR 28-JUL-2000; 2000US-00628127.

PA (ZYMO) ZYMOGENETICS INC.

PI Presnell SR, Conklin DC, Novak JE, Hammond AK;

DR WPI; 2003-897570/82.

DR N-PSDB; ADG87459.

PT New polynucleotide, useful for preparing a composition for treating e.g. anemia encodes a zalphall polypeptide cytokine receptor.

PS Claim 1; SEQ ID NO 2; 91pp; English.

CC The present invention relates to new isolated polynucleotide encoding
CC α aliphall polypeptide. The polynucleotide is useful for treating anaemia.
CC The invention is useful for producing α aliphall polypeptide and producing
CC an antibody to α aliphall polypeptide. The present sequence is human
CC α aliphall protein.

SQ Sequence 538 AA;

Query Match 100.0%; Score 2958; DB 7; Length 538;

Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGWAPLLLLLQGGWGCBDVCYTDYLQTVICILEMWNHPSTLTLLTWQDQYEELKD 60

Db 1 MPRGWAPLLLLLLQGCGWGPCDLVCYTYDYLQTVICILEMWNLHPSTLLTLTWQDDQYEELKD 600

61 EATSCSLHRSAHNATHATYTCHMDVEFHEMADDIFSVNITDQSGNYSQECGSFLAESIKP 120

Db 61 EATSCSLHRSAHNATHATYTCMDVFHFMADDIFSVNITDQSGNYSQECGSFLAESIKP 120

121 APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPWAVSPRKLISVDS 180

Db 121 APPFNVTVTFSGQYNISWRSDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRKLISVDS 180

181 RSVSLPLEFRKDSSYLEQVRAGPMPGSSYQGTWSEMSDPVIFQTQSEELKEGWNPHLL 240

Db 181 RSVSLPLEFRKDSYELQVRAGPMPGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLL 240

241 LLLLVIFIPAFWSLKTHPLWRLWKIWA VSPSPERFFMPLYKGCSDFKKWGAPFTGSS 300

Db 241 LLLVIVFIPAFWSLKTHTPLWRLWKIWA VPSPERFFMPLYKGCSDFKK WVGAF TGS 300

301 LELGWSPEVPSTLEVYSCHPPRSPAKRLQTELQEPALVESDGVPKPSFWPTAQNCGG 360

Db 301 LELGFWSPVPSTLEVYSCHPPRSPAKRLQTLTELQEPALVESDGVPKPSFWPTAQNCGG 360

QY 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCEDDGYPALDL DAGLEPSGLEP LLD 420

Db 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCEDDGYPALDLLAGLEPSPGLEDP LLD 420

421 AGTTLVSCGCVSAGSPGLGGLDRLKPLADGEDWAGGLPWGGRSPGCVSESEAGS 480

Db 421 AGTTVLSCGCVSAGSPGLGGLSLDLRLKPLADGEDWAGGLPMGGRSPGCVSESEAGS 480

481 PLAGLMDTFDSGFVGSDCSSPVECDFTSPGDEGPPRSYLKQWVI PPPLSSPGQAS 538

Db 481 PLAGLMDTFDSCGFVGSDCSSPVECDFTSPGDEGPFRSYLRQWVIPPPLSSPGPQAS 538

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:45:21 ; Search time 39.1971 Seconds
(without alignments)
1320.622 Million cell updates/sec

Title: US-10-659-684-115

Perfect score: 2958
Sequence: 1 MPRGWAPLILLLILGGWGC.....YLRQWVIPPPLSSPPQAS 538Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	278	9.4	551	2 A30342	interleukin-2 rece
2	249	8.4	537	2 B46535	interleukin-2 rece
3	247.5	8.4	539	2 A35052	interleukin-2 rece
4	233	7.9	896	1 A35782	cytokine receptor
5	221.5	7.5	468	2 A45268	interleukin-9 rece
6	218.5	7.4	878	1 A40091	interleukin-3 rece
7	215	7.3	522	2 B45268	interleukin-9 rece
8	213.5	7.2	467	2 B45268	gene gfi-2 protein
9	213	7.2	508	1 ZUHUR	erythropoietin rec
10	211.5	7.2	896	2 B45268	interleukin-3 rece
11	204	6.9	897	1 A39255	cytokine receptor
12	201	6.8	507	1 A32385	erythropoietin rec
13	195	6.6	507	1 A46713	erythropoietin rec
14	193.5	6.4	825	1 A60386	interleukin-4 rece
15	189.5	6.4	810	1 A33380	interleukin-4 rece
16	171	5.8	348	2 UC7907	common cytokine re
17	168.5	5.7	635	2 A45266	MP-1 protein prec
18	168.5	5.7	800	1 S31575	interleukin-4 rece
19	168	5.7	369	2 B45268	interleukin-2 rece
20	164.5	5.6	579	2 B45266	MP-1 protein prec
21	159	5.4	831	2 J01655	prolactin receptor
22	157	5.3	625	2 S35317	hematopoietic grow
23	157	5.3	626	2 S37622	proto-oncogene - m
24	151.5	5.1	805	2 S68441	leptin receptor, s
25	151.5	5.1	892	2 S68439	leptin receptor, s
26	151.5	5.1	894	2 S68437	leptin receptor, s
27	151.5	5.1	900	2 S68440	leptin receptor, s
28	151.5	5.1	1162	2 S68438	leptin receptor, s
29	146	4.9	459	2 A34791	interleukin-7 rece

30	144	4.9	373	2 A55718	interleukin-2 rece
31	143.5	4.9	459	2 D34791	interleukin-7 rece
32	143	4.8	369	2 A42565	interleukin-2 rece
33	139.5	4.7	298	2 B34791	interleukin-7 rece
34	139	4.7	895	2 S74225	leptin receptor, l
35	139	4.7	1162	2 PC4184	leptin receptor, O
36	135.5	4.6	954	1 S68178	mixed-lineage prot
37	128.5	4.3	284	2 S27931	Env/-mp1 fusion p
38	128.5	4.3	918	2 A44257	interleukin-6 sign
39	126.5	4.3	917	2 I49699	glycoprotein 130 -
40	125	4.2	262	2 C34791	interleukin-7 rece
41	123	4.2	295	2 A44984	collagen - nematod
42	123	4.2	468	1 A41242	interleukin-6 rece
43	123	4.2	1744	2 S40991	collagen alpha 1(I
44	122.5	4.1	420	2 S21052	interleukin-5 rece
45	121.5	4.1	2124	2 A28452	proteoglycan core

ALIGNMENTS

RESULT 1

A30342
interleukin-2 receptor beta chain precursor - human
N;Alternate names: CD25 beta chain
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A30342
R;Hakkeyama, M.; Teudo, M.; Minamoto, S.; Kono, T.; Doi, T.; Miyata, T.; Miyasaka, M.;
Science 244, 551-556, 1989
A;Title: Interleukin-2 receptor beta-chain gene: generation of three receptor forms by cl
A;Reference number: A30342; MUID:89242117; PMID:2785715
A;Accession: A30342
A;Molecule type: mRNA
A;Residues: 1-551 <HMT>
A;Cross-references: UNIPROT:P14784; UNIPARC:UP1000000128F; GB:M26062; NID:G186322; PIDN:J
C;Genetics:
A;Gene: GDB:112RB
A;Cross-references: GDB:118822; OMIM:146710
A;Map position: 22q11.2-22q13
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: cytokine receptor; transmembrane protein
F;1/26/Domain: signal sequence #status predicted <SIG>
F;27-551/Product: interleukin-2 receptor beta chain #status predicted <MAT>

Query Match	9.4%; Score 278; DB 2; Length 551;
Best Local Similarity	26.0%; Pred. No. 3.8e-12;
Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;	
QY	5 WAAPLILLL-LOGGW-----GCPDLVCTDYQLQVYICLLEMMNHLPSITLTLTWQOYE 56
DB	8 WRPLILLLPLPLATWSAAVNGTSQPTCFYNSRANISCV-----WS-----ODG 52
QY	57 ELDEATSCSLH-----RSANAT-----HATYTCM-----DVHFMDIDFSVNTD 100
DB	53 ALQD--TSCQVHMAPDRRRNQTCLELPVSQASACALLIGAPDSQTLTVDTITLVLC 110
QY	101 QSGNYSQECG--SFLLAESIKPAPFNVTVTF--SGQYNISWSDYEDPAPYMLKGLQY 156
DB	111 REGVRWVMAIQPKPFENRLMAPISLQVHVHETHCNISWEI---SQASHYERHLEF 167
QY	157 ELOYRNGDPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQVRAGPMGSSYQGTWSE 216
DB	168 EARTLSFGHTWEAP--LTLTKOKQWICLETLPDPTQYEFQVRVPLQGEF--TTWSP 222
QY	217 WSPVIRFQTSSEBKEG--WNPHILLLLLLVIFIPAPWSL-----KTHPLMRLLM-KKIW 268
DB	223 WSGPLARTRPAALGKOTIPMLGHLVGLSGARGFILVTLINCRNTCP---WLKKVL 278
QY	269 A--VPSPERFPMPLLYKCGSDPFKKWVGAPFTGSLBELGPMSPPEVPSLTLEYVSCHPSPSPA 326
DB	279 KCMTPDPSKFFSQSLSHSGDVGKMLSSPFPSSSFSFGGLAPEL-SPLEV-----L 328

[illegible]

RESULT 2

I:Interleukin 2 receptor beta chain - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
 C:Accession: B46535
 R:Page, T.H.; Dailman, M.J.
 E:Eur. J. Immunol. 21, 2133-2138, 1991
 A:Title: Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha and beta chains
 A:Reference number: A46535; MUID:91364784; PMID:1889461
 A:Accession: B46535
 A:Status: Preliminary
 A:Scatun: A
 A:Molecule type: mRNA
 A:Residues: 1-537 <PAG>
 A:Cross-references: UNIPARC:UPI000017987A
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBI:60818, NCBI:60819)
 C:Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
 I:Keywords: cytokine receptor

Query Match	8.4%	Score	249;	DB 2;	Length	537;
Best Local Similarly	23.5%	Pred.	No. 4.2e-10;			
Matches 148;		Conservative	70;	Mismatches	177;	Indels 234;
				Gaps		34;

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QY      5 WAAPL-LLLLLOGGW-----GCPDLVCYTDYIQTGYI CLEEMNNLHPSLTLLTWDQOYE 56
Db      8 WRLEPLYLILLLLATTTWVAANVDCSHLKCFYNSRANVSC-----MMS-----49
QY      57 ELKOE- --TSCSLHRSAH-----NAT-----HATYCHM-----DVHFHMDI FSV 96
Db      50 --PEEALNVTSCHLHAKSDMRHWNKTCELTEPVROASMACNLLIPLPDSGLTVDLLST 107
QY      97 NIT--DOSGNVSOECGSLFLAESIKPAPFVWVYTF--SGOYINSMR-----SDYEDAFY 148
Db      108 SVVWEKEMKMRVYTCNHFPPDNURLIAPHSLQVLHETRCNLSWEYSQVSHYVNP--- 164
QY      149 MLKGLQYELQYRNRRGDPWAVSPRRKLI SVDSRSVSLPLEFRK-----DSSYEL 198
Db      165 -----YLEBE-----ARRLLDRSMDASVSLKQROQWI FLETLPTDTSYEL 207
QY      199 QVRAGPMPGSSYOGTWSEKSDPVI FOTOSSELKXGNPHLLILLLYIVFLPAWS--- 254
Db      208 QVRVIAQRGKT--RTWSEWSQPMAFRTRPADPKEIFPLPWLRCULLYVLCGFFGLSCVCV 265
QY      255 -----LKTHPLWRLWKKI WAVSPERFMPPLKYGSSGPFKKVGA PF----- 296
Db      266 LVKCRYIYGPWLKTLKKCH-----IDPSEFSSQLSSQHGGLQKWLSSVPQSF 314
QY      297 ---TGSSLELCPMSPPEVSTLEVYSCHPRPSPARLOLTQEPALVELVESHGVPKPSFWP 353
Db      315 FSPFGSAPETISP-----LEVL D-----RDSKTMQMLLFQK-----EKASSPSP--- 353
QY      354 TAONSGSVAISEERDRPYGLVSI DTVTYVLDAGEGCTW---PC--SCEDDGYALDLDA 406
Db      354 --GHSQASCFNTQ-----GYFFPHLSNALTIESCOVYFYYPDPCMEDEVEDBG-DRLEBES 405
QY      407 GLBE-----SPGLBEDPLDAGTVLSCGCVSAGSPGLGRL-----GSLDLRL 449
Db      406 PLPLPLPFTGEQDDYCAFPFRDLDLL-----FSPSLSTPNATYAGNSITPEE 451

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QY      450  KPRLAAGGEWMAAGLPPGCGRRPGCVSEASGAPLGLMDTRDSDGFGVSDCSSPVCFTS  509
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      452  RPPPLSLQF-----GLP-----SLASDLMGL-----QHRELEBL--  480
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      510  PGDEGPPRSYLROWVIVPPPLSSPGPPQAS  538
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      481  -GDDEGQMS-----TNSSGQQAAS  497
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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RESULT 3

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interleukin-2 receptor beta chain precursor - mouse
C|Species: Mus musculus (house mouse)
C|Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #ext_change 09-Jul-2004
C|Accession: A35052
R|Kono, T.; Doi, T.; Yamada, G.; Hatakeyama, M.; Mimamoto, S.; Tsudo, M.; Miyasaka, M.; N
Proc. Natl. Acad. Sci. U.S.A. 87, 1806-1810, 1990
A|Title: Murine interleukin 2 receptor beta chain: dysregulated gene expression in lympho
A|Reference number: A35052; PMID:90175385; PMID:215425
A|Accession: A35052
A|Status: Preliminary
A|Statut: preliminary
A|Molecule type: mRNA
A|Residues: 1-539 <KON>
A|Cross-references: UNIPROT:P16297; UNIPARC:UPI0000003F2c; GB:W28052; NID:gl98313; PIDN:;
C|Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
|Keywords: cytokine receptor; transmembrane protein

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Query Match	8.4%	Score 247.5	DB 2	Length 539
Best Local Similarity	23.7%	Pred. No. 5.5e-10		
Matches 138; Conservative	68;	Mismatches 198;	Indels 179;	Gaps 29

[illegible]

RESULT 4

A35782
Cytokine receptor common beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A35782
R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreure, J.; Yonehara, S.; Yahara, I.; Arai, K.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like protei
A:Reference number: A35782; MUID:90319131; PMID:1695379
A:Accession: A35782
A:Molecule type: mRNA
A:Residues: 1-896 <GCR>
A:Cross-references: UNIPROT:P26955; UNIPARC:UPI000002785; GB:M34397; NID:9191821; PIDN:
C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 recept
C:Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-896/Product: cytokine receptor common beta chain #status predicted <WAT>
F:23-441/Domain: extracellular #status predicted <EXT>
F:23-235/Domain: cytokine receptor homology <CRS1>
F:233-434/Domain: cytokine receptor homology <CRS2>
F:442-463/Domain: transmembrane #status predicted <TM>
F:464-896/Domain: intracellular #status predicted <INT>

Query Match 7.9%; Score 233; DB 1; Length 896;
Best Local Similarity 20.4%; Pred. No. 1.1e-08;
Matches 113; Conservative 86; Mismatches 220; Indels 134; Gaps 23;

Qy 22 DLVCTYLQTVLCILEMWN-----LHPTLTLTWQDYELKDEATCSLHRS 70
Db 250 NLQGFPGIGISLHSMWETQTGSVSGCLFRRSPVA-----PEEKCPVYKRP 299
Qy 71 AHNATHATYTCMDVFFHMADDFISVNTDGSNGVSGCFLLA-ESIKRAPP-FNVTV 128
Db 300 PGASVYTRYHSLVPEPSAHSQYTVSK-----HLEQGFIMSYNHIQMEPTLNLTK 353
Qy 129 TFSQVNVMSRDVEDPAFYMLKGLQYELQYRRNGDPWASPPRKLSVDSRSVSLPL 188
Db 354 N-RDSYSLHMETQMAVSFT---EHTFQVQYKKKSDSWEDSKTENLDRAHSMDS--- 404
Qy 189 EFRKDSYELQVRAPMGSGSYQGTWSEWSDPVI.FQTQSEBELKEGWNPHLLLLLVVF 248
Db 405 QLEBDTSCARVKRPT--SNYDGIWMSKSEETWMT-DWMPPLMVLIVLFLITLTL 461
Qy 249 IPAFWSLKHPLMLWKIMAVSPERFFMPLVYGCSDGFKKWVGAPFTGSSLELGPWS 308
Db 462 ILRGCVSVTRYTKMKKE--KIPNPSKSL-----FQDGGKGLMP--- 499
Qy 309 EVPSTLEVYSGHRP--RSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSSGSAVSEE 366
Db 500 --PGSMAPFATKNALQPOSRL-LAEQ-----GESYVHL 532
Qy 367 RDRYGLVSDITVTVL--DAEGPCTWPCSCD--DGYPALDDAGLEPSPGLDPLDAG 422
Db 533 EDNNVSELTIEDPIIIVKPSGPDTPAASSESTEQLPNVYEGPTPRKPKQLEPSTP-- 590
Qy 423 TYVLSGCVSASGSLGSP---LGSLLDLRLKPLADGE---DWAGGLPMWGRSPG--- 472
Db 591 -----FNGPYLGRPGSHSLPDLPGSGPQVGGSLKRALPGSLLEYWCLAPGGQVQ 640
Qy 473 -----VSESEASPLAGLDMDTFDGSFVSDCSSPECCFTSPGDEGPRSTRLRQNV 525
Db 641 LVPLSQWGGQAMDVOCSSLETSGSPSVKPNPVELSMEOEARNDP----- 691
Qy 526 IPPPLSGPPOAS 538
Db 692 VTLPISSGGPRGS 704

RESULT 5
A45268
interleukin-9 receptor precursor - mouse
C:Species: Mus musculus (house mouse)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A45268
R:Renault, J.C.; Druez, C.; Kermon, A.; Housiau, F.; Uytendhoe, C.; Van Roost, E.; Ve
Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992
A:Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs.
A:Reference number: A45268; MUID:92302307; PMID:1376929
A:Accession: A45268
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-468 <REN>
A:Cross-references: UNIPROT:Q01114; UNIPARC:UPI000000057; GB:M4746; NID:9194044; PIDN:
A>Note: authors translated the codon GGG for residue 394 as Gln
C:Keywords: glycoprotein; receptor; T-cell proliferation; transmembrane protein

Query Match 7.5%; Score 221.5; DB 2; Length 468;
Best Local Similarity 23.2%; Pred. No. 3.3e-08;
Matches 134; Conservative 60; Mismatches 181; Indels 203; Gaps 34;

Qy 3 RGNAPPLLLLLQSGWG--CPDLVCTYDYLQTVLCILEMWNLHPTLTL-----TW----- 51
Db 36 RGVSVP-----EQGGGQKAGAPCLNSIYRDC-----HNSABELQESRAMLLFT 83
Qy 52 QDYELKDEAT-----SCSLHRSAHNA-----THATYTCMDVFFHMADDFISVNTDQSG 103
Db 84 SNQVTEIKHKCTPMDSNCTLVLPKEEVFLPNDFTTLHRCI---MGQE--QVSLVD--- 135
Qy 104 NYSQCCSFLAELSIKAPPNV-TVTFSGQYINSMDSYEDPAFYMLKGLQYELQYRN 162
Db 136 -----SQYLPRRHRIKIDPPSDLOSNSVSGCVLTWGINL--ALEPLITSLSYELAFKR 186
Qy 163 RGDPMWASPPRKLSVDSRSVSLPLLEFRKDSYELQVRA-----GPMGSSYQGTW 214
Db 187 QEEWENRKHDRIVGV--TWLILEAVLNPGSIYEAALRQMTLESYEDKTEGEYYSHW 244
Qy 215 SEMSDPVI.FQTQSEBELKEG-----WNPHLLLLLVIFIPAFWSLK--THPLMRL-- 263
Db 245 SEMGQPSF--PSQGRQGLLVPRWQWSAIL-----VVVPIFLLTGFWHLFLKSP 295
Qy 264 -WKIM--AVSPERFFMPLVYGCSDGFKKWVGAPFTGSSLELGPWSEVSTLEVYSGH 320
Db 296 RLKRI.FQNIIPSPAPFPHPLYSVYHGDFOSTGTGRRAG----- 333
Qy 321 PPRSPAKRLQLTLEQPAELVESDGVKPSFWPTAQNSSGSAVSEERDRPYGLVSI- 376
Db 334 -----PARKQVSTSGSBS-----SIW 353
Qy 377 DTVTVLDAEGPCTWPCSC-----EDDGYPALDDAGLEPSPGLDPLDAGTVLSCGV 431
Db 354 EAVATLTVSPACPVQFACLKMEATAPGPGI-----PGSEH-----VLPAQCL 396
Qy 432 S-AGSPGLGPRGLSLDLRLKPLADGEDWAGLEPMWGRSPGVSEASGSPLAGLDMDTF 490
Db 397 ELEQPSAVLP-----QEDWA---PLGSARP--PPDSDSGS----- 428
Qy 491 DSGFVSDCSSPVGCDFTS--RGDEGPRSTRYLQWVVP 527
Db 429 -SDYCMLDCE--ECHLSAPFGHTSEPLTLQEPVALP 463

RESULT 6
A40091
interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A40091; A43022
R:Itoh, N.; Yonehara, S.; Schreure, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara, I
Science 247, 324-327, 1990
A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene
A:Reference number: A40091; MUID:90117145; PMID:2404337
A:Accession: A40091
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-878 <ITO>

A/Cross-references: UNIPROT:P26954; UNIPARC:UPI000015742D
 R:Gorman, D.M.
 Submitted to GenBank, November 1989
 A/Reference number: A43022
 A/Accession: A43022
 A/Molecule type: mRNA
 A/Residues: 1-815, 'O', 817-878 <GOR>
 A/Cross-references: UNIPARC:UPI000020F33; GB:M29855; NID:g198342; PIDN:AA39295.1; PID:
 C/Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains a
 receptor.
 C/Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
 C/Keywords: cytokine receptor; duplication; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-878/Product: interleukin-3 receptor beta chain #status predicted <EXT>
 F:23-440/Domain: extracellular #status predicted <EXT>
 F:33-238/Domain: cytokine receptor homology <CRS1>
 F:254-463/Domain: cytokine receptor homology <CRS2>
 F:441-462/Domain: transmembrane #status predicted <TM>
 F:463-878/Domain: intracellular #status predicted <INT>

Query Match 7.4%; Score 218.5; DB 1; Length 878;
 Best Local Similarity 21.5%; Pred. No. 1.2e-07;

Matches 119; Conservative 79; Mismatches 219; Indels 137; Gaps 25;

OY 22 DLVCTVTLQTVICILEMNLHPSTLTWQDYELKDEATSCSLHRSANATHATVTC 81
 Bb 251 NLQGFPGIQLHSCWEWMTTGSVRLGFLYRSPAPREKCSFVYKVEQASVYTRRC 310
 OY 82 HMDVFHFMADDFSVNITDQSGVSOECGFLLA-ESIKPAPFNVTVTFSGQYNISMS 140
 Bb 311 SLVPESASAHQVTVSVK-----HLEQKFMISYHVIQMEPILNQTKNDSYSLHET 364
 OY 141 D-----YDDPAPYMLKGLQYELQYRNCDPMAVSPRRKLISVDSRSVLLLEFRKSSY 196
 Bb 365 QKIPKYIDHTF-----QVYKKKSESXKSKXTENLGRVNSMD--LF-QLEPDTSY 411
 OY 197 ELQVAPMPGSSSYQGTWSESDVIFQTOSEELKEGW-NPHLLLLLVIVIFIPA----- 251
 Bb 412 CARRVKPI--SDVDGIMSEWSNEYWTTD-----WVMTLWIVLILVILITLALL 462
 OY 252 -FMSLKTPLRLKLTWAVSPERFEMPLKYGCGSGDFKVVAGAPFTGSSLELGPWSEV 310
 Bb 463 HFGVYVYRTYRKWE--KIPNPSKSL-----FQDGGKLMF----- 498
 OY 311 PSTLEVYCHRP--RSPAKRLQLTLEQ-----EPALVESGVKPKSFWPTAQ 356
 Bb 499 PGSAAPATYKXNPAALQGPQSRLLAEQGVSYEHLNENNSPLTIEDPIIDP--BSRP 554
 OY 357 NSGSAVSEERDRPYGLVSDITVTVLDAEGPCPTWPCSCEDDGYPALDLADGLESPGLE 416
 Bb 555 DTPPAASE-----STEQLENVVEGPI--PSSRPKQLPSFDN-----GPYIGP 598
 OY 417 PLLDAGTTVLSGCVSAGSPGLGSLGS--LLDLKPLADGEDMAGGLPMGSSPGG-- 472
 Bb 599 P-----QSHSLPDLPGQLGSPQVGSGLKPLA-----PSGLBYMCLPPEGQV 639
 OY 473 -----VSESEKGPLAGLDMPTFDSGFVSGSCSSPVECDTSPDEGPRRYLQWV 524
 Bb 640 QLVPLSQVMGGQMDVQCGSSLETGSPSYEPKPNPVEKQEARDPNMTL----- 694
 OY 525 VIPLPLSPGPQAS 538
 Bb 695 -----PISSSGPEGS 704

RESULT 7

B45268
 interleukin-9 receptor precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C/Accession: B45268
 R:Renauld, J.C.; Druet, C.; Kermouni, A.; Housseau, F.; Uytendhoe, C.; Van Roost, E.; V
 Proc. Natl. Acad. Sci. U.S.A. 89, 5690-5694, 1992

A/Title: Expression cloning of the murine and human interleukin 9 receptor cDNAs.
 A/Reference number: A45268; MUID:92302307; PMID:1376929
 A/Accession: B45268
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-522 <REN>
 A/Cross-references: UNIPROT:Q01113; UNIPARC:UPI000016AAD3; GB:M84747; NID:g184508; PIDN:
 C/Keywords: glycoprotein; receptor; T-cell proliferation; transmembrane protein

Query Match 7.3%; Score 215; DB 2; Length 522;
 Best Local Similarity 24.9%; Pred. No. 1.1e-07;

Matches 137; Conservative 52; Mismatches 200; Indels 162; Gaps 33;

OY 35 CILEMNLHPSTLTWQDYELKDEATSC-----SLHRSANATHATVTC 80
 Bb 6 CIMEGWLSEBALRDMGTW-----LLACICCTCVCLGVSTYGCGGRSTFT 55
 OY 81 C-----HMDVFHFMADDFSVNITDQSGV-----SQECGFLLAESIKP 120
 Bb 56 CLTNMILRIDC-HMSAPDELQGGSSPMLFTSN-QAPGTHKCLRGSECTVLPPEAVL- 112
 OY 121 APPENVTVTF-----SCQYINISW-----RSDE-----DPAF 147
 Bb 113 VPSDNFTITPHCMVSGREQVSLVDPEYLPRRHVCLDPPSDLQSNISSGHCILTWSISPAL 172
 OY 148 YMLKGLQYELQYRNCDPMAVSPRRKLISVDSRSVLLPLE-FRKDSY-----ELQVRA 202
 Bb 173 EPMITLLSYELAPKQGEAMQOHRDHY-----GVYMLLEAFELDPGFIHEARLAVQM 228
 OY 203 GPMFG-----SYQGTWSESDVIFQTOSE-----LKEGMNPHLLLLLVIVIFPAFW 253
 Bb 229 ATLEDVVEERYTQGWSEWSQPCFOAPQPGPLIPPMGMPGN--TLVAVSIFL----- 281
 OY 254 SLKTHPLRLM-----KLTW--AVSPERFEMPLKYGCGSGDFKVVAGAPFTGSSLE-- 302
 Bb 282 -LITGPYLLFKLSPRVKRIFYQNVBPAPMFQPLVSVHNGFQTMWGAARAGVLLSQDC 340
 OY 303 -----LGPWSEVSTLEVYCHPSPAKRLQLTLEQ-----PALVESDGVPKPSFW 352
 Bb 341 AGTPQGLPEFCVQETATLLTCGPAP--PKSVALLSEBEGCTRLPGULSSEVDVLPAGC-- 397
 OY 353 PTAONSGSAVSEERDRPYGLVSDITVTVLDAEG--PCTWPCSCEDDGYPALDLADG-- 407
 Bb 398 -TEWRVQTLAYLPQED--MAPTSLTRPAPDSEGSRSSSSSSNNNNNCALGCVGWH 454
 OY 408 LBSPPGLE-----PLLDAGTTVLSG-----GCYSAG--SPGLGPGSLDLDR 448
 Bb 455 LSALEPNTQSSGPIPALACG--LSCDHQGLTQGVAVWVLAGHCORPGLHEDLQGL-- 509
 OY 449 LKPLADGEDM 459
 Bb 510 LPSVLSKARSW 520

RESULT 8

156896
 gene gfi-2 protein - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: 156896
 R:Flubacher, M.M.; Bear, S.E.; Teichlis, P.N.
 J. Virol. 68, 7709-7716, 1994
 A/Title: Replacement of interleukin-2 (IL-2)-generated mitogenic signals by a myk cell f
 ed leukemogenesis.
 A/Reference number: 156896; MUID:95055995; PMID:7966560
 A/Accession: 156896
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-467 <RES>
 A/Cross-references: UNIPROT:Q63216; UNIPARC:UPI0000086943; GB:L36459; NID:g598371; PIDN:
 C/Genetics:
 A/Gene: gfi-2

Query Match 7.2%; Score 213.5; DB 2; Length 467;
 Best Local Similarity 22.0%; Pred. No. 1.2e-07;
 Matches 115; Conservative 61; Mismatches 179; Indels 167; Gaps 25;

15 OGGKGCPLVCTYDTQVTCILEMMNLHPSTLTLM-----QDYEELKDEAT-----SCS 66
 44 EGRKACATTCFCFSNSVRIDC---HMSA-PEPGRALLFTSNCTDICKKCTWDSRCT 99
 67 LHRSAHNA-----THATYTCNMDVHFMAADIFSVNITDQSGNYSQEGCSFLLAESIKPAP 122
 100 LVLPKEKAPLFPDFMTITLHRCV---MQQE---QVSLVD-----SQYLPRRHILKDP 145
 123 PENV-TYTFSGQNNISMSRSDVEDPAFYLKKLOLEYQYRMRGDPMAVSPRKLISVDSR 181
 146 PSDIQSVSSGRCVLTWGISF---GLEPLTSLSYELAFKQOEAWE-QAQLKRIQVGT 201
 182 SVSLPLPEFRKDSSEYELQVRA-----GPMSSYQGTWSEWSDPIVFTQSEELKEG 233
 202 WLVLKALELNDPTIYEARLRYQMLSEYDCKTEBEYKSKHSEWSQSVSFSPRKTQG- 260
 234 WNPRLLLLLL-----VIVTIPAFWSLK--THPLMRWKI-----WAVSPERPFM 278
 261 -----LLIPRQGSASILVAVPIFULLTGLIHPFLSPKVKRIFYQVVPSPAPFFH 312
 279 PLYKGCSDPRKXWGAPFTGSLLELGPMSPEVPTLAVYSGHPRSPAKRLQLTELQEP 338
 313 PLYSVYHGFQFTWIGARRAG----- 332
 339 ELVESDGVPRKSPFPTQNSGASAYSEERDRPYGLVSDITVTLDAEGPTCPWSCDDG 398
 333 -----PQKRDGASAPSGDSE-----SIMEALATLTYSACSVQ- 367
 399 YPALDLDAGLEPSEGLDPLLDAGTIVLSCGVAS-AGSPGLGRLGSLDLRLKPLADGE 457
 368 FPLSLKWA---TANGPFGP--PGSELVLPAGCLLEQPSAYLP-----QE 408
 458 DMAGGLPWGGRPGCVSESEAGSFLAGLNDTSPSGFYGSDC 499
 409 DMA---PLGSARP-----PPLSDSGSSDYCMDC 435

RESULT 9
 ZUHUR
 erythropoietin receptor precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 12-Feb-1993 #sequence revision 05-Apr-1995 #text change 09-Jul-2004
 C:Accession: A43799; A60160; A49824; A53958; A55280; A52563
 R:Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.
 Blood 76, 31-35, 1990
 A>Title: Human erythropoietin receptor: cloning, expression, and biologic characterization
 A:Reference number: A43799; MUID:90304340; PMID:2163696
 A:Accession: A43799
 A:Molecule type: mRNA
 A:Residues: 1-508 <JUN>
 A:Cross-references: UNIPROT:P19235; UNIPARC:UPI000012A0AD; GB:M60455; NID:9182244; PIDN:
 R:Minkelman, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.
 Blood 76, 24-30, 1990
 A>Title: The gene for the human erythropoietin receptor: analysis of the coding sequence
 A:Reference number: A60160; MUID:90304334; PMID:2163695
 A:Accession: A60160
 A:Molecule type: not compared with conceptual translation
 A:Molecule type: mRNA; DNA
 A:Residues: 1-101; R', 103-188, 'R', 103-188, 'E', 245-508 <WIN>
 A:Cross-references: UNIPARC:UPI00001736C2
 R:Noguchi, C.T.; Bae, K.S.; Chin, K.; Wade, Y.; Schechter, A.N.; Hankins, W.D.
 Blood 78, 2548-2556, 1991
 A>Title: Cloning of the human erythropoietin receptor gene.
 A:Reference number: A49824; MUID:92399733; PMID:1668606
 A:Accession: A49824
 A:Molecule type: DNA
 A:Residues: 1-508 <NOG>
 A:Cross-references: UNIPARC:UPI000012A0AD; GB:S45332; NID:9255496; PIDN:AA23271.1; PID:
 A:Experimental source: Placenta

A>Note: sequence extracted from NCBI backbone (NCBIN:113293, NCBIPI:113294)
 R:Ettemann, K.; St. John, T. 1991
 Exp. Hematol. 19, 973-977, 1991
 A>Title: The erythropoietin receptor gene: cloning and identification of multiple tranac
 A:Reference number: A53958; MUID:91372359; PMID:1654273
 A:Accession: A53958
 A:Molecule type: mRNA
 A:Residues: 1-508 <EHR>
 A:Cross-references: UNIPARC:UPI000012A0AD
 R:Penny, L.A.; Forget, B.G.
 Genomics 11, 974-980, 1991
 A>Title: Genomic organization of the human erythropoietin receptor gene.
 A:Reference number: A55280; MUID:92147143; PMID:1664413
 A:Accession: A55280
 A:Molecule type: DNA
 A:Residues: 1-17,381-387, 'LLEQQA', 391-395,504-508 <DEN>
 A:Cross-references: UNIPARC:UPI000016A8A4; UNIPARC:UPI00001736C3; UNIPARC:UPI00001736C4
 A>Note: sequence modified after extraction from NCBI backbone
 A>Note: the authors translated the codon GAT for residue 31 as B
 R:Mouché, L.; Touramille, C.; Hattab, C.; Boffa, G.; Cartron, J.P.; Chretien, S.
 Blood 78, 2557-2563, 1991
 A>Title: Cloning of the gene encoding the human erythropoietin receptor.
 A:Reference number: 152563; MUID:92399734; PMID:1668607
 A:Accession: 152563
 A>Status: translated from GB/EMBL/DBEJ
 A:Molecule type: DNA
 A:Residues: 1-96 <RES>
 A:Cross-references: UNIPARC:UPI000016A8A4; GB:M76595; NID:9182147; PIDN:AAA52393.1; PID:5;
 C:Genetics:
 A:Gene: GDB:EBOR
 A:Cross-references: GDB:125242; OMIM:133171
 A:Map position: 19p13.3-19p13.2
 A:Intons: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
 C:Superfamily: erythropoietin receptor; cytokine receptor homology
 C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-508/Product: erythropoietin receptor #status predicted <MAT>
 F:52-250/Domain: extracellular #status predicted <EXT>
 F:52-239/Domain: cytokine receptor homology <CRS>
 F:233-237/Region: MSXMS motif
 F:251-272/Domain: transmembrane #status predicted <TM>
 F:273-508/Domain: intracellular #status predicted <INT>
 F:52-62,91-107/Distalide bonds: #status predicted
 F:76/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 7.2%; Score 213; DB 1; Length 508;
 Best Local Similarity 21.6%; Pred. No. 1.5e-07;
 Matches 127; Conservative 63; Mismatches 175; Indels 224; Gaps 30;

9 LLLLLLGGWGP-----DLVCYDYLTQVTCILE---MNNLHP 44
 15 LCLLLAGAAWAPPNLDPKFEKALLLAARGPEELCTFERLEDVLCFMEBAASAGVGP 74
 45 STLTLTQDQDEELKDEAT-CLHRSANHATATYTCM-----DVTFMADDFSVNITD 100
 75 GNSVSFYQ-----LEDEPMLCRHQAPTARGAVFCSLPTADTSSFPV---LELRVTA 126
 101 OSGNVSQEGCSFLLAESIKAPFNVTF-----SQQYVMSRSD 141
 127 ASG-----APRYHRYIHNEVVLDPAGVLARLADBSGHVLRPLP 169
 142 YEDPAFMYLKGLOLEYQYRMRGDPMAVSPRKLISVDSRVSLLPLEFRKDSSEYELQV 201
 170 PEP-----MTSHRVEYDVASGAGAGSV---QVEILEGRTCVLS-NLGRRTYTPAVR 221
 202 AGPMPSSTYQGTSEWSDPIVFTQSEELKEGMNPHLL--LLLVVTFIPAFWSLTKTP 259
 222 A-RMAEBSFGFWMSAMEPVSLLTPSD-----LDPLTLTSLILVILVTLVALLSHR 275
 260 LMRLMKKI-WAVSPERPFMPLYKGCSDGDFKXV-----GAPFTGSSLELGPMSPEVSTL 314
 276 R-ALKQKIMPGIISPESEFGLFTTHKGNQLMLYONDCLW-----WSCTPFTTE 325

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QY 315 EYVSCHPRSPAKRLQLTLEQPAELVESDGVPKPSFWPTAONGSGAYSEERDRPYGLV 374
D 326 D-----PPAS-----LEVTSERC-----MGTVQ----- 343
QY 375 SIDTVTVLDAEGPCTWPCSCEDDYPALDLADLEPSPGLLEDPLDAGTTLVSCGVASAG 434
D 344 AVERGT--DDEGPLLEFVGSEHADDTLVLDKMLPR----- 378
QY 435 SPGLGGLGSLDLRLKPPPLADGEMAGGLPWGGRSPGVSEASGSLAGLDMDTPPSGF 494
D 379 -----NPPSEB-----LP-----GPGG-----SVDIVAMDEGS 401
QY 495 VGSPPSCSPVECDFTSPGDEG-----PPRSYLROWVPI--PP 529
D 402 EASSCSALA---SKPSPEGASAFETYITLDPSSQLRPWTLCPELRP 447

RESULT 10
156563
interleukin-3 receptor beta-subunit - rat
C/Species: Rattus sp. (rat)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-May-2004
C/Accession: 156563
R/Apple, K.; Buttin, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A/Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and
A/Reference number: 156563; MUID:95370942; PMID:7643220
A/Accession: 156563
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-896 <RES>
A/Cross-references: UNIPARC:UPI000008999A, GB:S79263; NID:G1086954; PIDN:AB3506.1; PID
A/Genetic:
A/Gene: rIL-3beta
C/Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
C/Keywords: cytokine receptor
F/3-235/Domain: cytokine receptor homology <CRS1>
F/253-433/Domain: cytokine receptor homology <CRS2>

Query Match 7.2%; Score 211.5; DB 2; Length 896;
Best Local Similarity 21.7%; Pred. No. 3.8e-07;
Matches 126; Conservative 79; Mismatches 228; Indels 147; Gaps 28;

QY 2 PRGNAALULLLLLOGGCP-----DLVCTDYDTQVTCILEMNLHPSSTLTLMQD 53
D 229 PSCGSPV-----HWDSPTEKARPONLCQCFDGIQSLNCSWEVWTKVTDVSFGLFY 281
QY 54 QYELKDQEATSCSLHRAAHNATHATYTCMDVFFHMAADDIPSVNITDQSGNYSQEGCSFL 113
D 282 SSSPKAGEKCSFVVKELQASRYTRYHCSLNSDPAHSSQYTVSVK-----RLQCKFI 335
QY 114 LA-ESIKPAPP-FNVTVTFSGQYNIISWSDYEDPAFYWLKGLQYELQYRNRRGDPWAVSP 171
D 336 ESFNHIQNPPTLNLTKN-RDSYSLHWETQMSYPI----QHAFOYQKKKLLRMEDESK 390
QY 172 RKRLISVDSRSVSLPLRFKDSYELQYRAGPMGSSYQGTWSEMSDPVIFQOSEBK 231
D 391 TENINHAHSMQ--LP-QLEPGTSYCARVRKTIIP-EYKLMSEWSSECTWTDD----- 439
QY 232 EGM-NPHL---LILLVIVPIPA--FWSLTHPLMLMKIMAVSPSPERFPMLYKCS 285
D 440 --WMPFLMVLIVLITLTLRLFCIGCYKLRMKKINPSSLLFQGGKGL- 496
QY 286 GDFKRWGAPFTGSLGLPMSPEVPSTLEVYSCHP-PRSPAKRLQLTLEQPAELVESD 344
D 497 -----WPP--GSTVTFSSKNPFPQGPQNL-FSELQ----- 524
QY 345 GVKPSFWPTAONGSGAYSEERDRPYGLVSDIVTVL--DAEGPCTWPCSCEDDYPAL 402
D 525 -----GVSYTHLEDNVSPLTIEDPNIIRDPSSGPDTPPAASSBP----- 564
QY 403 DLADGLEPSPGLE-DPLLDAGTTLVSCGVASGSPGLGGL-----GSLLD-----R 448
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D 565 -----MEQSSNVQVDPPTLSGRPRKQLPSEDFNGPYLGPQSHSLDLPQLVPGVGS 619
QY 449 LKRPPLADGEDMAGGLPWGGRSPG-----VSESEAGSLAGLDMDTPDGFVGS 498
D 620 LKRAL-----PSLSELMCLPFGGQVOLVPLSCVWKCQGRDVQDCSSLETSPSESR 673
QY 499 CSSPVECDFTSPGDEGPPRSYLROWVPIPPPLSSPPQAS 538
D 674 ESPPELV-----KEEBOEPKRN-----PYTLPISSGGPKXS 704

RESULT 11
A39255
cytokine receptor common beta chain precursor - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-May-2004
C/Accession: A39255
R/Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A/Title: Molecular cloning of a second subunit of the receptor for human granulocyte-mac
A/Reference number: A39255; MUID:91086571; PMID:1702217
A/Accession: A39255
A/Status:
A/Molecule type: mRNA
A/Residues: 1-897 <HAY>
A/Cross-references: UNIPARC:UPI00001736C0; GB:M38275
C/Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific
C/Genetic:
A/Gene: GDB:CSF2RB
A/Cross-references: GDB:126838; OMIM:138981
A/Map position: 22q13.1-22q13.1
C/Superfamily: cytokine IL-3/IL-5/GM-CSF receptor common beta chain; cytokine receptor h
C/Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protein
F/1-16/Domain: signal sequence #status predicted <Sig>
F/11-897/Product: cytokine receptor common beta chain #status predicted <MAT>
F/17-443/Domain: extracellular #status predicted <EXT>
F/35-232/Domain: cytokine receptor homology <CRS1>
F/250-431/Domain: cytokine receptor homology <CRS2>
F/444-460/Domain: transmembrane #status predicted <TM>
F/461-897/Domain: intracellular #status predicted <INT>

Query Match 6.2%; Score 204; DB 1; Length 897;
Best Local Similarity 22.6%; Pred. No. 1.3e-06;
Matches 142; Conservative 66; Mismatches 219; Indels 200; Gaps 32;

QY 22 DLVCTDYDTQVTCILEMNLHPSSTLT--LTMDQYBELKDEATSC-----SLHSAH- 72
D 247 NLCCFPDGAVALVSCSWEVRKEVASVSGFLFYRSPDAGEECSPLYREGLSLHTRHHC 306
QY 73 -----NATHATYTCMDVFFHMAADDIPSVNITDQSGNYSQEGCSFLAESIKPAPPNV 126
D 307 QIYVPDATHGQY-----IVSY-----QPRRAEKHKHKS---SYNIGMAP--SL 345
QY 127 TVTFSG-QYNIISW-----RSYEDPAFYWLKGLQYELQYRNRRGDPWAVSPRKLISVDS 180
D 346 NVTKQDGSYSLSRWETMKRYEHIDHTF-----EIQYKDTATWKDSKTEYL--QNA 394
QY 181 RVSLSLPLERKSSYELQYRAGPMGSSYQGTWSEMSDPVITQOSEBKDEGNPHLL 240
D 395 HSMALPALE--PSTRWARVRV-RTSRTGNGTWMSESESRSDTES--VLPMW----- 443
QY 241 LILLVIVPIPA-----FWSLTHPLMLMKIMAVSPSPERFPMLYKCSGDFPKW-- 291
D 444 VIALIVIFLTTAVLALRFGIGYLRMRKMEKINPSSLSHLPQ-----NSAELMPP 497
QY 292 --VGAPFTGSLGLPMS--PEV-----PSTLE--VYSCHPSPAKRLQ 330
D 498 GMSAFTSGSPRPQGPWGRFPELGVFPVGFDSSEVSLTIBDPKHVCDPSPGPDTPPA 557
QY 331 LTELQPAELVESDGVPKPSFWPTAONGSGAYSEERDRPYGLVSDIVTVLDAEGCTW 390
D 558 ASDLPTEQPPSPQGPAAASHTEKQASS-----FPNNGVYL 595
```

```

Qy 391 P---CSCEDD-GYPALDLADGLEPSP---GLEPDLIDAGTTVLSCGCVSAGSPGIG---- 439
Db 566 PPHSHSLPDLIGQPPPEGGSGQSPPEGSLEYLCLPAGGQVQLVPLAQMGPGQAVVE 655
Qy 440 -----GPIGLSLDLRLKPPPLADGEDWAGGLPMWGRSP-----GGVSESEAGSPLAGLDM 487
Db 666 RRPQGAAGS-----PGLSESG-----GGPAPPLAGPRVGGQDQKDSVALPMSSG 700
Qy 488 DTFPSGFLVSGDCSPVECDFT-----SPGDEGPP 516
Db 701 DTEDEG-VASGYVSADLVFTPNSGASVSLVSLGLPSDQTPSLCPGLASGPPGAPGV 759
Qy 517 RSYLRQWVIRP-----PLSSPPG 535
Db 760 KSGFEGVELPEPIEGRSPRSPRNVP 786

```

RESULT 12

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A32385
erythropoietin receptor precursor, membrane-bound form - mouse
C.Species: Mus musculus (house mouse)
C.Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C.Accession: A41686; A32385; S13249
R.Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A.Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
A.Reference number: A41686; MUID:92017832; PMID:1656233
A.Accession: A41686
A.Molecule type: mRNA
A.Residues: 1-507 <HIN>
A.Cross-references: UNIPROT:P14753; UNIPARC:UPI00000008997; GB:S59388; NID:g237036; PIDN:
A.Experimental source: murine erythroleukemia (MEL) cell line F5-5
R.D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989
A.Title: Expression cloning of the murine erythropoietin receptor.
A.Reference number: A32385; MUID:89195238; PMID:2539263
A.Accession: A32385
A.Molecule type: mRNA
A.Residues: 1-507 <DAA>
A.Cross-references: UNIPARC:UPI00000008997; GB:J04843; NID:g193090; PIDN:AAA37571.1; PID:
A.Experimental source: murine erythroleukemia (MEL) cells, subclone 745
R.Kuramoto, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A.Title: Characterization of murine erythropoietin receptor genes.
A.Reference number: S13249; MUID:91080149; PMID:2175360
A.Accession: S13249
A.Molecule type: DNA; mRNA
A.Residues: 1-507 <KID>
A.Cross-references: UNIPARC:UPI00000008997; EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:
A.Experimental source: murine erythroleukemia K-1 cells
C.Genetics:
A.Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
C.Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane protein
C.Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F.1-24/DNA: signal sequence #status predicted <SIG>
F.25-507/Product: erythropoietin receptor #status predicted <MAT>
F.25-249/DNA: extracellular #status predicted <EXT>
F.52-238/DNA: cytochrome receptor homology <CRS>
F.250-271/DNA: transmembrane #status predicted <TMM>
F.272-507/DNA: intracellular #status predicted <INT>
F.752-62,90-106/DNA: disulfide bonds #status predicted
F.75/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match 6.8%; Score 201; DB 1; Length 507;
Best Local Similarity 23.1%; Pred. No. 1e-06;
Matches 117; Conservative 60; Mismatches 188; Indels 142; Gaps 27;

```

```

Qy 2 PRGMAAPLLLLLLGCGW-----GCPDLVCYTDYLTQVICILEMW 40
Db 10 PR--VGPICLLLAGAAMAPSPSLPDPKESKALLASRGSEBELCFTORLEDLVCFWE-- 65
Qy 41 NLHPSLTLLTQDOYEELEKDEATCSLSRSHNATHATYTCHM---DVHFHMADDIIFSVN 97

```

```

Db 66 EAASGMDENYSFSYQLEGEGRKSCSLHQAPTVRGVRFWCSLPADTSSFPV---LELQ 122
Qy 98 ITDOSGN--YQO-----EGCSFLAAS-----IKPAPFNVTYTFSGQYNIS 137
Db 123 VTEASGSPRYHRIIHINEVLLDAPAGLLARAEBSHVLRWLPFGAPMTTHIRYEV- 181
Qy 138 WRSDVEDPAFMFLMGKQLQYELQYNRGDPMAVSPRKLISVDSRVSLLPLEFRKSSYE 197
Db 182 -----DVASGR-----AGCQRVEVEGRRECLLS-NLRGCTRYT 216
Qy 198 LQVAPGMPGSSYQGTWSEMSDPVYFQTOSEELKGNPHLLLLLVIVIRP--AFWS 254
Db 217 FAVRA-RWAEPSFSGFWSAMEPASILTAAD-----LDP-LILTLSTLIVLISLLTVIA 269
Qy 255 LKTHPLWRLMKIIV-AVSPERFPMPLTKGSGGDFKKV---GAPFGSSLELGNAPPE 309
Db 270 LLSHRH-TLOOKIWPGLIPSPSEFEGLFTTHKGNFQWLRLORDCLW-----WSPG 319
Qy 310 VPSITLEVYSCHPSPSPARQLQTLQEPALVESDGPV-----KPSFMTAONSGSAY- 363
Db 320 -----SSPEDEPA--HLEVISEPRMAVTOAGDGADEGLLEPVSGEHAQDTYL 368
Qy 364 -----SEERDPYGLVSDITVYLDAGPCTWPCSCEDDGYPALDLADGLEPS 411
Db 369 VLDRKWLPRTPCSENLSPGCG--SVDPYTMEASSTSCPSDLSKRP-----EGTSPS 421
Qy 412 PGLDEPLLDAGTTVLSCGCVSAGSPGL 438
Db 422 -SFEYTLIDPSSQLL---CPRALPPEL 444

```

RESULT 13

```

A46713
erythropoietin receptor precursor - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: A46713
R.Maeda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasaki,
J. Biol. Chem. 268, 11208-11216, 1993
A.Title: Functional erythropoietin receptor of the cells with neural characteristics. Cc
A.Reference number: A46713; MUID:93265574; PMID:7684373
A.Accession: A46713
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-507 <MAS>
A.Cross-references: UNIPROT:Q07303; UNIPARC:UPI000012A0AE; GB:D13566; NID:g286209; PIDN:
A.Experimental source: PC12 and erythroid cells
A.Note: sequence extracted from NCB1 backbone (NCBI:132813, NCBIR:132813)
C.Superfamily: erythropoietin receptor; cytokine receptor; glycoprotein; transmembrane protein
C.Keywords: cytokine receptor; glycoprotein; transmembrane protein
F.1-24/DNA: signal sequence #status predicted <SIG>
F.25-507/Product: erythropoietin receptor #status predicted <MAT>
F.52-238/DNA: extracellular #status predicted <EXT>
F.250-271/DNA: cytochrome receptor homology <CRS>
F.272-507/DNA: transmembrane #status predicted <TMM>
F.75/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match 6.6%; Score 195; DB 1; Length 507;
Best Local Similarity 21.4%; Pred. No. 2.8e-06;
Matches 126; Conservative 70; Mismatches 194; Indels 198; Gaps 32;

```

```

Qy 2 PRGMAAPLLLLLLGCGW-----GCPDLVCYTDYLTQVICILEMW 40
Db 10 PR--VSPICLLLAGAAMAPSPSLPDPKESKALLASRGSEBELCFTORLEDLVCFWE-- 65
Qy 41 NLHPSLTLLTQDOYEELEKDEATCSLSRSHNATHATYTCHM---DVHFHMADDIIFSVN 97
Db 66 EAASGMDENYSFSYQLEGEGRKSCSLHQAPTVRGVRFWCSLPADTSSFPV---LELQ 122
Qy 98 ITDOSGN--YQO-----EGCSFLAAS-----IKPAPFNVTYTFSGQYNIS 137
Db 123 VTEASGSPRYHRIIHINEVLLDAPAGLLARAEBSHVLRWLPFGAPMTTHIRYEV- 181

```

Qy 138 WRSDYEDPAFYMLKGLQYELQYENRGDPAVSPRRKLISVDSRSVSLPLEFRKDSYE 197
Db 182 -----DVASAGNR-----AGTORVELEGRETCVLN-ILHGRTYTT 216
Qy 198 LQYRAGMPGSSGYOTSEMSDPIVIFOTOSSELEKEGNPHLLLLLVIVIFP---AFWS 254
Db 217 FAYVA-RMAERFSGFPMFSAMSEPAISLTASD-----LDP-LILVLSLIVLISLLTAYLA 269
Qy 255 LKTHPLRLMKKIV-AVPSPERFMPLYKCGSGDFKVV-----GAPFTGSSLEIGPMSP 309
Db 270 LLSHRR-ALROKIPGIPSPENEFEGUFTTHKGNFQMLLQORDCLW-----WSPS 319
Qy 310 VPSLTLEYVSCHPMSPAKRIQLTLOEPAELVESGVKPSFMPYTAQNSGGSAVSEERD- 368
Db 320 SPF-----PDDPAHLEVLSERR-----KGYTQ--AGDAGAEKGP 353
Qy 369 --RPYGLV-SIDYTVTLDAEGPCTW-----PCSGEDDGYPALDLDALEPSPLEDPLLD 420
Db 354 LLEBVGSEBRADYTLVID-----EMLPRCPCSNLSS-----PGDSVDPATMD 397
Qy 421 AGTTVLSGCVSAGSPGLG-----PLGSLI-DRLKPLADGEDMAGGLPWG 467
Db 398 EGSETSSCPSDIASKPRPEGTSPSFEYTLIDPSKSLCPRALPP----- 442
Qy 468 RSPGVSSEKASP-LAGLMDTFDPSGFGVSGSDCSSPVCEPFTSPQDEG 514
Db 443 -----ELPPTPHLKLYLVVSDSG-----ISTDYSSGSGSQ 474

RESULT 14

A60386 interleukin-4 receptor precursor - human

N/Alternate names: IL-4 receptor
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

A/Accession: A60386; MUID:91120547; PMID:2278997

R/Gilzai, J.P.; Zubur, C.E.; Harada, N.; Gorman, D.M.; Djoseu, O.; Kastelein, R.; Banc

Int. Immunol. 2, 669-675, 1990

A/Title: Molecular cloning of a cDNA encoding the human interleukin 4 receptor.

A/Reference number: A60386; MUID:91120547; PMID:2278997

A/Accession: A60386

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-825 <GAL>

A/Cross-references: UNIPROT:P24394; UNIPARC:UPI0000169C06

R/Idzerda, R.L.; March, C.J.; Mosley, B.; Lyman, S.D.; Vanden Bos, T.; Gimpe, S.D.; Dir

J. Exp. Med. 171, 861-873, 1990

A/Title: Human interleukin 4 receptor confers biological responsiveness and defines a nc

A/Reference number: A47603; MUID:90171849; PMID:2307934

A/Accession: A47603

A/Molecule type: mRNA

A/Residues: 1-74, 'I', '76-825 <ID2>

A/Cross-references: UNIPARC:UPI0000044371; GB:X52425; NID:G33833; PIDN:CAA3672.1; PID:G

C/Genetics:

A/Gene: GDB:1148

A/Cross-references: GDB:118823; OMTM:147781

A/Map position: 16p12.1-16p12.1

C/Superfamily: interleukin-4 receptor; cytokine receptor homology

C/Keywords: cytokine receptor; glycoprotein; transmembrane protein

F/1-25/Domain: signal sequence #status predicted <SIG>

F/26-85/Product: interleukin-4 receptor #status predicted <MNT>

F/26-232/Domain: extracellular #status predicted <EXT>

F/34-218/Domain: cytoplasmic receptor homology <CRS>

F/223-256/Domain: transmembrane #status predicted <TM>

F/257-825/Domain: intracellular #status predicted <INT>

F/53,98,128,134,146,209/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.5%; Score 193.5; DB 1; Length 825;

Best Local Similarity 21.8%; Pred. No. 6.6e-06;

Matches 161; Conservative 69; Mismatches 220; Indels 289; Gaps 42;

Qy 17 GMGCPDLV-----CTDYLQVYICILMMNLHNPST-----L 47

Db 2 GMILSGSLIFPVSCVLTLQVASSGNMKVLQEPCTVSDYMSISTC---EMKNAGPTNCSTEL 58
Qy 48 TLTWQDQYELKQBATSCSLHRSANATHATYCHMDVHFPMADIFSVNITQSGNYSQ 107
Db 59 RLIVYQLVF--LLEBAHC-----VPENNAGAGCVCHL-----LMDVVASD-----NYTL 101
Qy 108 EC-----GSFLAESIKPAPPFNVTV--TFSGQYNISWRSDYEDPAFYMLKGLQY 156
Db 102 DLNAGQOLMKKGFKEBENHKKPAPGULTVHTVNSDTLLLTWNSPY--PEDNVLNHLTY 159
Qy 157 ELOYRNGDPAVSPRRKLISVDSRSVSLPLB-----FRKSSYELQYRAGMPG 207
Db 160 AVNWSEND-----ADFRIYNTVYLEPSLRIAASTLKSGISYARAVRAM---A 205
Qy 208 SSTQGTSEMSDPIVIFOTOSSELEKEGNPHLLLLLVIVIFIPAFMSLKHPLRLMKKI 267
Db 206 QCVNTWSEMSPTKMH--NSYREPEQHLHGVSVSCIVILAVCLLCVYSTIKIKKEW 262
Qy 268 W-AVSPERPFM-----PLYKGC-----S 285
Db 263 WDIQIPNAPKRLVAIIIQDAQSGSWEKRSRGEPKACPHKNCULYLPCELEHMKRDE 322
Qy 286 GDFKRWGAPFTGSSSLELGPWP-EV-----PSTLEVYSCHPRPSPAKRLQLTLOE-P 337
Db 323 DPHKAKEMFQSGG--KSAMCPVEISKVTLWPEISISVVC-----VELFEAP 368
Qy 338 AELVESGV--PKSPFMPYTAQNSGGSAVSEERDPRVGLVSDYTV-LDAG----- 386
Db 369 VECEEEVEEKEGSPFCASSPSSRD--FOEGRE--GIVARLTSLPLDLLEENGSGFCQ 424
Qy 387 -----PCTWPCSCED-----DGYPALDLDAE-----LEPSPG----- 413
Db 425 QDMGESCLLPSPSGSTSHMWPDEPFS---AGFEKAPMKGEQPHLEPPSPASPTQSPD 480
Qy 414 ----LEDPILDAGTV--LSCGCVSAGSPGLGP--LGSLLDRLKP----- 451
Db 481 NLCTEFTPLVIAGNPAVRSFNSLSQSPCRELDGPDLLARHLEVEPEMPCVQLSEPT 540
Qy 452 --PLADSEDM-----AGGLPMGRSRG---GVSESEAG-----SPPLGL----- 485
Db 541 TVDPPEPETEQLIRNVLQHGAAAPVAPSTGYOEFVNAVQGTQASAVVGLGPGE 600
Qy 486 -DMOTPDGFGVSGSCSPVECDFTS-----PDDEGPPRSYLQWVIP 527
Db 601 AGYKAF--SSILASANSPEKCGFASGEGYKPFQDLIGCFEDDPAP-----VP 649
Qy 528 PLSSPG-----PGAS 538
Db 650 VPLFTFGLDREPPSPQSS 668

RESULT 15

A33380 interleukin-4 receptor precursor - mouse

N/Alternate names: IL-4 receptor

C/Species: Mus musculus (house mouse)

C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

A/Accession: A33380; B33380; C33380; A34861; I54232

R/Mosley, B.; Beckmann, M.P.; March, C.J.; Idzerda, R.L.; Gimpe, S.D.; VandenBos, T.; F

Widmer, M.B.; Coeman, D.; Park, L.S.

Cell 59, 335-348, 1989

A/Title: The murine interleukin-4 receptor: molecular cloning and characterization of seq

A/Reference number: A90911; MUID:90030408; PMID:2805066

A/Accession: A33380

A/Molecule type: mRNA

A/Residues: 1-810 <MO1>

A/Cross-references: UNIPROT:P16382; UNIPARC:UPI000004194; GB:M27959; NID:G198363; PIDN:J

A/Accession: B33380

A/Molecule type: mRNA

A/Residues: 1-258 <MO2>

A/Cross-references: UNIPARC:UPI00001736C1

A:Molecule type: mRNA
 A:Residues: 1-224, 'PSNENTL', <MO3>
 A:Cross-references: UNIPARC:UPI0000136CL; GB:M27960; NID:g198365; PIDN:AAA39300.1; PID:
 A>Note: part of this sequence, including the amino end of the mature protein, was confir
 A>Note: three forms of cDNA were isolated; the longest encodes extracellular, transmembr
 A:Note: domain and may encode a soluble form of the receptor
 R.Harda, N.; Castle, B.E.; Gorman, D.M.; Itoh, N.; Schreure, J.; Barrett, R.L.; Howard,
 Proc. Natl. Acad. Sci. U.S.A. 87, 857-861, 1990
 A:Title: Expression cloning of a cDNA encoding the murine interleukin 4 receptor based c
 A:Reference number: A34861; MID:90138976; PMID:2405398
 A:Accession: A34861
 A:Molecule type: mRNA
 A:Residues: 1-810 <HAR>
 A:Cross-references: UNIPARC:UPI000004194; GB:M29854; NID:g198346; PIDN:AAA39297.1; PID:
 R.Wright, N.C.; Campbell, L.A.; Lee, F.D.
 Growth Factors 6, 103-118, 1992
 A:Title: The murine interleukin-4 receptor gene: Genomic structure, expression and pote
 A:Reference number: 154232; MID:92265335; PMID:1534014
 A:Accession: 154232
 A:status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-73, 'I', '75-333', 'P', '335-810' <RES>
 A:Cross-references: UNIPARC:UPI00000655CA; GB:M64879; NID:g198359; PIDN:AAB59727.1; PID:
 C:Genetics:
 A:introns: 24/1; 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2
 C:superfamily: interleukin-4 receptor; cytokine receptor homology
 C:keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-810/Product: interleukin-4 receptor #status predicted <EXT>
 F:26-233/Domain: extracellular #status predicted <EXT>
 F:234-219/Domain: cytokine receptor homology <CRS>
 F:234-257/Domain: transmembrane #status predicted <TM>
 F:258-810/Domain: intracellular #status predicted <INT>
 F:72,129,135,163,177/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 6.4%; Score 189.5; DB 1; Length 810;
 Best Local Similarity 20.9%; Pred. No. 1.3e-05;
 Matches 159; Conservative 70; Mismatches 222; Indels 309; Gaps 42;

QY 9 LLLLLLQGGWGCPLD---VCYTYLQTVICILEMWNH-----PSTLTTLTQDOYEELKD 60
 DB 15 LILLVLTGSGSIVLGGPTCFPSDIYRSTC---EMFLDSAVDCSQCLHYRLMFFEFSE 71
 QY 61 EATSCSLHRSANATATYTCGMDVFRHMADIFSVNITQSGNYSQEC-----GS 111
 DB 72 NLTCI-----PRNSASTVCVCHME-----NMRPVQSDRYQWELWAHROLWQGS 115
 QY 112 FLAASIKPAPPPNVTV--TFSGQYNISMRSDY-----EDPAPYML 150
 DB 116 FSPSGNVKPLAPNLTHTNVSDEMLTNNLTPSNLLYKDLISMVNIREDNPAPFIV 175
 QY 151 KGLQYELQYRNKGPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQVRAGPMGSSY 210
 DB 176 ---YNYTYK---EPRLSPINILMS-----GVYTYARVR---VRSQIL 209
 QY 211 QGTWSEKSDVITFOTGSEELKEGNPHLLLLL-----LVVTFPAFWSLKTPLMR 262
 DB 210 TGTWSEWSPSIT-----WYNHFOPLIQRPLGVITISCLCPLCLFCYFSITX 258
 QY 263 LMKKIW--AVSPERPFM-----PLYKGC-----284
 DB 259 I-KKIWMDOQPTPARSPVAIIITQDAQVPLMDKQTRSQSESTKYPHWKTCLODKLPCLLKH 317
 QY 285 ---SGDFKMGVAGPFTGSSLLELGP--WSP-EVPSLTLEVYSCPPRSPAKRLQTELQE- 336
 DB 318 RVKKKTDPRK--AAP-TKSLQSPGKAGCMHEVSRIV---LWPENVSVSVRCMELFEA 370
 QY 337 PAELV--ESGCVKPSFWPTAQNSSGSAYSB-ERDRPYGLVSDITVTLDAE----- 385
 DB 371 PVQNVBEEDIEIVKEDLSMSPENGGCGFQSSQADIMARLTENLFSDLLEAENGLQCSA 430
 QY 386 -----GCTWPC-----SCDDGVPALEDLDAGLSPSPGLBDDPLDAG 422

DB 431 LAESCSPLPSGSGQASVSWACLPMPGPSEBATTQVTEQPS-----HPGRLSGSPAQAP 483
 QY 423 TTVLSSG-----CVSAGSPGLGGPILSLDRLK-----450
 DB 484 T-LACTQVPLVADNPAYRFSFDCSPAPNPGELAPBEOQADHLEEEPPSPADPHSSG 541
 QY 451 PPLADGEDW-----AGG--LPMWG-----RSPGVSESEAGSP 481
 DB 542 PPMQPVESMEQLIHMSVLQHGAAAGSTPAPAGGYQGFVQAVKQGAADPEVGPVRPSGDP 601
 QY 482 -----LAGLMDT---FDSGFVG-----SDCSSPYECDFT-----508
 DB 602 GYKAFSSILSSNGIRGDTAAAGTDDGHGGYKPFQNPVPNQSPSSVPL---FTGLDTELS 658
 QY 509 -SPGDGPPRSTYLR-----QWVYIPPLSS--PGP 535
 DB 659 PSLNSDPPKSPPECUGLEIGLKGDWVXAPPPADQVFKP 698

Search completed: September 7, 2006, 12:52:23
 Job time : 43.1971 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 7, 2006, 12:40:11 ; Search time 296.669 Seconds
(without alignments)
1677.489 Million cell updates/sec

Title: US-10-659-684-115

Sequence: 1 MFGMAAPLILLLLQGSGWC.....YLRQWVITPPPLSSPQNAS 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92505592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 7.2:*
1: UniProt_sprot:*
2: UniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2958	100.0	538	IL21R_HUMAN	O9HBE5 homo sapien
2	1735.5	58.7	529	IL21R_MOUSE	O9JH33 mus musculu
3	1735.5	58.7	529	O3TA13_MOUSE	O3TA13 mus musculu
4	1734.5	58.6	529	O3UBS8_MOUSE	O3UBS8 mus musculu
5	1703.5	57.6	521	O5EBH1_RAT	O5EBH1 rattus norv
6	1082	36.6	292	O3TA82_MOUSE	O3TA82 mus musculu
7	872	29.5	268	O6FEU8_MOUSE	O6FEU8 mus musculu
8	764	25.8	590	O5F4A6_CHICK	O5F4A6 gallus gall
9	294	9.9	551	IL2RB_MACFA	O38J85 macaca fasc
10	286	9.7	512	O6UAP3_TETNG	O6UAP3 tetraodon n
11	280	9.5	551	IL2RB_PANTR	O38J84 pan troglod
12	278	9.4	551	IL2RB_HUMAN	P14788 homo sapien
13	261	8.8	509	O2VB08_BRARE	O2VB08 brachydanio
14	250	8.5	890	O9Z1A0_CAVPO	O9Z1A0 cavia porce
15	248	8.4	537	IL2RB_RAT	P68996 rattus norv
16	247.5	8.4	539	IL2RB_MOUSE	O3T2C2 mus musculu
17	247.5	8.4	539	O3TR72_MOUSE	O3TR72 mus musculu
18	246.5	8.3	539	O3TR02_MOUSE	O3TR02 mus musculu
19	245.5	8.3	539	O8R308_MOUSE	O8R308 mus musculu
20	243.5	8.2	539	O8CB01_MOUSE	O8CB01 mus musculu
21	239.5	8.1	539	O4KKX7_MOUSE	O4KKX7 mus musculu
22	233	7.9	896	IL3RB_MOUSE	P26955 mus musculu
23	231	7.8	896	O3U7L5_MOUSE	O3U7L5 mus musculu
24	231	7.8	896	O8QZK9_MOUSE	O8QZK9 mus musculu
25	231	7.8	896	O3U2T6_MOUSE	O3U2T6 m nod-deriv
26	227	7.7	896	O3U109_MOUSE	O3U109 mus musculu
27	226	7.6	529	O6UAP7_TETNG	O6UAP7 tetraodon n
28	221.5	7.5	468	IL6R_MOUSE	O01114 mus musculu
29	221.5	7.5	468	O78P55_MOUSE	O78P55 mus musculu
30	221.5	7.5	631	O6UANA4_TETNG	O6UANA4 tetraodon n
31	221.5	7.5	878	O3U1W0_MOUSE	O3U1W0 mus musculu

ALIGNMENTS

32	221.5	7.5	878	2	O3U241_MOUSE	O3U241 m nod-deriv
33	218.5	7.4	439	2	O6UANA4_TETNG	O6UANA4 tetraodon n
34	218.5	7.4	769	2	O3U1Z1_MOUSE	O3U1Z1 mus musculu
35	218.5	7.4	790	2	O3U3P4_MOUSE	O3U3P4 mus musculu
36	218.5	7.4	878	1	IL3B2_MOUSE	P26954 mus musculu
37	215	7.3	522	1	IL3B2_HUMAN	O01113 homo sapien
38	213.5	7.2	467	2	O63216_RAT	O63216 rattus norv
39	213	7.2	508	1	EPOR_HUMAN	P19235 homo sapien
40	213	7.2	508	2	O2M205_HUMAN	O2M205 homo sapien
41	211.5	7.2	896	2	O64146_9MURI	O64146 rattus sp.
42	211.5	7.2	896	2	O782F5_RAT	O782F5 rattus norv
43	210	7.1	459	2	O8C2G1_MOUSE	O8C2G1 mus musculu
44	208.5	7.0	652	2	O3U2L4_MOUSE	O3U2L4 mus musculu
45	208.5	7.0	670	2	O3TB34_MOUSE	O3TB34 mus musculu

RESULT 1	IL21R_HUMAN	STANDARD;	PRT;	538 AA.
ID	IL21R_HUMAN			
AC	O9HBE5; O96H21; O9HB91;			
DT	02-MAY-2002, integrated into UniProtKB/Swiss-Prot.			
DT	01-MAR-2001, sequence version 1.			
DT	07-MAR-2006, entry version 47.			
DE	Interleukin-21 receptor precursor (IL-21R) (Novel interleukin receptor).			
GN	Name=IL21R; Synonyms=NILR; ORFNames=UNQ3121/PRO10273;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;			
RA	Parrish-Novak J., Dillon S.R., Nelson A., Sprecher C.,			
RA	Grosz J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,			
RA	Burkhead S., Heipel M., Brandt C., Kuiper J.L., Kramer J.,			
RA	Corklin D., Pressnell S.R., Berry J., Shiohara F., Bort S., Hamblly K.,			
RA	Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,			
RA	Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,			
RA	Mauser W., Kaushansky K., Holly R.D., Foster D.;			
RT	"Interleukin 21 and its receptor are involved in NK cell expansion and			
RT	regulation of lymphocyte function.";			
RL	Nature 408:57-63 (2000).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=20481926; PubMed=11016959; DOI=10.1073/pnas.200360997;			
RA	Ozaki K., Kikly K., Michalovich D., Young P.R., Leonard W.U.;			
RT	"Cloning of a type I cytokine receptor most related to the IL-2			
RT	receptor beta chain.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444 (2000).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Bruen J.,			
RA	Chen J., Chow B., Chu C., Crowley C., Currell B., Denel B., Dowd P.,			
RA	Baton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,			
RA	Huang A., Klam H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Matk M.R., Robble E., Sanchez C., Schoenfeld J.,			
RA	Sehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,			
RA	Yanusa D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,			
RA	Wood W.I., Godowski P.J., Gray A.M.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment.";			
RL	Genome Res. 13:2265-2270 (2003).			
RN	[4]			
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS CYS-191; ARG-318 AND			
RP	SER-484.			

RA Bieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Peel C.L., Foch E.V., Yi Q., Nickerson D.A.,
 RT "SeattleSNP: NHLBI HUG6682 program for genomic applications, UW-
 RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>).
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=B-cell, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krauseberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krauseberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Saplanton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrincci P., Prange C.,
 RA Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."/
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP PROTEIN SEQUENCE OF 20-34.
 RX PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.,
 RT "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites."/
 RL Protein Sci. 13:2819-2824(2004).
 CC -1- FUNCTION: This is a receptor for interleukin-21.
 CC -1- SUBUNIT: Heterodimer with the common gamma chain. Associates with
 CC JAK1.
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein.
 CC -1- TISSUE SPECIFICITY: Selectively expressed in lymphoid tissues.
 CC Most highly expressed in thymus and spleen.
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation.
 CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
 CC
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 CC
 CC EMBL: AF254067; AAC29346.1; -; mRNA.
 CC EMBL: AF269133; AAC23419.1; -; mRNA.
 CC EMBL: AY358826; AAQ89185.1; -; mRNA.
 CC EMBL: AY064474; AAL39168.1; -; Genomic_DNA.
 CC EMBL: BC004348; AAH04348.1; -; mRNA.
 CC EMBL: BC007946; AAH07946.2; -; mRNA.
 CC HSSP: P19235; 1EBA.
 CC Ensembl: ENSG00000103522; Homo sapiens.
 CC H-InvDB: HIX00121913; -.
 CC HGNC: HGNC:6006; IL21R.
 CC MIM: 605383; gene.
 CC GO: GO:0016021; C:integral to membrane; NAS.
 CC GO: GO:0001532; P:interleukin-21 receptor activity; NAS.
 CC GO: GO:0030101; P:natural killer cell activation; NAS.
 CC InterPro: IPR003531; FN_III.
 CC InterPro: IPR003531; FN_III.
 CC InterPro: IPR003531; FN_III.
 CC PROSITE: PS50853; FN3; FALSE NEG.
 CC PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.

KW Direct protein sequencing; Glycoprotein; Membrane; Polymorphism;
 KW Receptor; Signal; Transmembrane.
 FT SIGNAL 1 19
 FT CHAIN 20 538
 FT
 FT TOPO_DOM 20 232
 FT TRANSMEM 233 253
 FT TOPO_DOM 254 538
 FT DOMAIN 120 209
 FT MOTIF 214 218
 FT CARBOHYD 73 73
 FT CARBOHYD 97 97
 FT CARBOHYD 104 104
 FT CARBOHYD 125 125
 FT CARBOHYD 135 135
 FT DISULFID 25 35
 FT DISULFID 65 81
 FT VARIANT 191 191
 FT
 FT VARIANT 318 318
 FT
 FT VARIANT 484 484
 FT
 FT CONFLICT 386 386
 FT SEQUENCE 538 AA; 59130 MW; 414079CCB974850A CRC64;
 Query Match 100.0%; Score 2958; DB 1; Length 538;
 Best Local Similarity 100.0%; Pred. No. 7,8e-203;
 Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPKGMAAPLLLLLLGGGMCGLDVCYTDYQYICILEMNNLHPSTLTLMQOYEELKD 60
 DB 1 MPKGMAAPLLLLLLGGGMCGLDVCYTDYQYICILEMNNLHPSTLTLMQOYEELKD 60
 QY 61 EATSCSLHRSANAHATATYTCNDVDFHFNADIFSVNITDQSGNYGECGSLFAESIKP 120
 DB 61 EATSCSLHRSANAHATATYTCNDVDFHFNADIFSVNITDQSGNYGECGSLFAESIKP 120
 QY 121 APPENVTVTSSGOYNTSMRSYDIEDPAFYMLKGLQYELQYRNKGDPVAASPRKLISVDS 180
 DB 121 APPENVTVTSSGOYNTSMRSYDIEDPAFYMLKGLQYELQYRNKGDPVAASPRKLISVDS 180
 QY 181 RSVSLPLERKSSVELQYRAGPMGSSSYQGTWSEMSDVIRQTOSEELKEGNPHLL 240
 DB 181 RSVSLPLERKSSVELQYRAGPMGSSSYQGTWSEMSDVIRQTOSEELKEGNPHLL 240
 QY 241 LLLLVTFIPAFMSLKTHTPLMLKKIWAAPSEBEPMPDYKCGSGDFKMGVGAFTGSS 300
 DB 241 LLLLVTFIPAFMSLKTHTPLMLKKIWAAPSEBEPMPDYKCGSGDFKMGVGAFTGSS 300
 QY 301 LEIGPMSPEVPSLTLEVYSGCHPPSPAKRQLTLEQEAALVESDGVKBSFWPAAQNSCG 360
 DB 301 LEIGPMSPEVPSLTLEVYSGCHPPSPAKRQLTLEQEAALVESDGVKBSFWPAAQNSCG 360
 QY 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCWPCGCEDDGYPALDADLSPGLEDPLD 420
 DB 361 SAYSEERDRPYGLVSTDTVTVLDAEGPCWPCGCEDDGYPALDADLSPGLEDPLD 420
 QY 421 AGTTVLSGCVSAGSPGLGPIGLSLDLRLKPLADGDMWAGLPMWGRSPGVSEBAGS 480
 DB 421 AGTTVLSGCVSAGSPGLGPIGLSLDLRLKPLADGDMWAGLPMWGRSPGVSEBAGS 480
 QY 481 PLAGLMDTFTDSCGVSGDCSSPVBCDFTSGDGGPPRSYLRQWVVIPLPLSSRQPAQS 538
 DB 481 PLAGLMDTFTDSCGVSGDCSSPVBCDFTSGDGGPPRSYLRQWVVIPLPLSSRQPAQS 538
 RESULT 2
 ID IL21R_MOUSE STANDARD; PRT; 529 AA.
 AC Q9UHK3; Q9ESM1;
 DT 02-MAY-2002, integrated into UniProtKB/Swiss-Prot.

RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 RN (7)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Activated spleen;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwaigi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ND; TISSUE=Activated spleen;
 RA Arikawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Nishimura N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanishi A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
 CC -1 DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -1 DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC -----
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 CC -----
 CC EMBL: AK171826; BAF42685.1; -; mRNA.
 DR MGI: MGI:1890475; 1121r.
 DR GO: GO:0003998; F:acetylphosphatase activity; RCA.
 DR GO: GO:0004907; F:interleukin receptor activity; IDA.
 DR InterPro: IPR001792; Acylphosphatase.
 DR InterPro: IPR003531; Hemip rcptl_S_F1.
 DR PRINTS: PR00112; ACYLPHPTASE.
 DR PROSITE: PS01355; HEMATOPOI_REC_S_F1; UNKNOWN_1.
 DR KEGG: KEGG:01355; HEMATOPOI_REC_S_F1; UNKNOWN_1.
 KW Receptor; Transmembrane.
 SQ SEQUENCE 529 AA; 58355 MW; 8841816B0D426581 CRC64;
 Query Match 58.7%; Score 1735.5; DB 2; Length 529;
 Best Local Similarity 62.7%; Pred. No. 2e-115;
 Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;
 QY 1 MPRGMAAPLILLLLQGGWGPDPVLCYTDYDTOTVCIILEMMNLHPSTLTTLTQDOYEELKD 60
 DB 1 MPRGMAAPLILLLLQGGWGPDPVLCYTDYDTOTVCIILEMMNLHPSTLTTLTQDOYEELKD 60
 QY 61 EATSCSLHRSANATHTATYTCMDVFFHMADDFSVNTDQSGVNSGQSGFLLAESIKP 120
 DB 61 EATSCSLHRSANATHTATYTCMDVFFHMADDFSVNTDQSGVNSGQSGFLLAESIKP 120
 QY 61 QETFCSLHRSANATHTATYTCMDVFFHMADDFSVNTDQSGVNSGQSGFLLAESIKP 120
 DB 61 QETFCSLHRSANATHTATYTCMDVFFHMADDFSVNTDQSGVNSGQSGFLLAESIKP 120
 QY 121 APPNMTVTEGQVNIWSRSDYEDPAFMYLKGKLOEYQYNNRQDPMVAVSRKLISVDS 180
 DB 121 APPNMTVTEGQVNIWSRSDYEDPAFMYLKGKLOEYQYNNRQDPMVAVSRKLISVDS 180
 QY 121 APPNMTVTEGQVNIWSRSDYEDPAFMYLKGKLOEYQYNNRQDPMVAVSRKLISVDS 180
 DB 121 APPNMTVTEGQVNIWSRSDYEDPAFMYLKGKLOEYQYNNRQDPMVAVSRKLISVDS 180
 QY 181 RSVSLPLLEFRKDSYELQVAPGMPGSSYQGTWSEMDPIFOTQSEELKEGNNPHLL 240
 DB 181 RSVSLPLLEFRKDSYELQVAPGMPGSSYQGTWSEMDPIFOTQSEELKEGNNPHLL 240
 QY 181 RSVSLPLLEFRKDSYELQVAPGMPGSSYQGTWSEMDPIFOTQSEELKEGNNPHLL 240
 DB 181 RSVSLPLLEFRKDSYELQVAPGMPGSSYQGTWSEMDPIFOTQSEELKEGNNPHLL 240
 QY 241 LLLLVIVIFPAFWSLKHPLRLMKTKWA-VSPERFERFMPLYKCGSGDFKKVGAAPTGS 299
 DB 241 LLLLVIVIFPAFWSLKHPLRLMKTKWA-VSPERFERFMPLYKCGSGDFKKVGAAPTGS 299
 QY 241 LLLLVIVIFPAFWSLKHPLRLMKTKWA-VSPERFERFMPLYKCGSGDFKKVGAAPTGS 299
 DB 241 LLLLVIVIFPAFWSLKHPLRLMKTKWA-VSPERFERFMPLYKCGSGDFKKVGAAPTGS 299
 QY 300 STELGPMSPSEVSTLLEVYSCPPSPARRLDTLEQFAELVESDGVKPSFW---PTAO 356
 DB 300 STELGPMSPSEVSTLLEVYSCPPSPARRLDTLEQFAELVESDGVKPSFW---PTAO 356

DB 300 STELVPSSTTTAL-----HLSYPAKEKKFPGLPGLBEQLECDGMSEPGHWCIPLAA 354
 QY 357 NSGSAISEERDRRYGLVSDITVTYVLDAGEGCTTPCGCEDDGYALDLDALEPSGLIED 416
 DB 355 GOAVSAVSEERDRRYGLVSDITVTYVLDAGEGCTTPCGCEDDGYALDLDALEPSGLIED 414
 QY 417 PLDAGTTVSCGVSAAGPGLAGPLSLDRLKPLADGEDMAGGLPMGGRSPGVSES 476
 DB 415 LLLVTDPAFLSCGVSAAGPGLAGPLSLDRLKPLADGEDMAGGLPMGGRSPGVSES 474
 QY 477 EAGSPPLAGLMDTRDPSGFGVSDCSSPVCEFTSPGDEGPPRSYRQWVIPPPLSPQPO 536
 DB 475 EAGSP-PGLMDTRDPSGFGVSDCSSPVCEFTSPGDEGPPRSYRQWVIPPPLSPQPO 527
 QY 537 AS 538
 DB 528 SS 529
 RESULT 4
 Q3UBS8 MOUSE PRELIMINARY; PRT; 529 AA.
 AC Q3UBS8;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Bone marrow macrophage cDNA, RIKEN full-length enriched library,
 DE clone:1830015L18 product:interleukin 21 receptor, full insert
 DE sequence.
 GN Name=Il21r;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kaasakawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aldins V., Allen J.E., Bailey T.L.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgakilas-Hemmings P., Gingeras T.R., Gotohori T., Green R.E.,
 RA Gueniche S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Hummelnick L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Koillias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Farber S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Seesä S., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,

QY 181 RSVLLPLEFRKSSYELQVRAGMPGSSYOGTWSWSDPYIFOTQSEELKEGNPHLL 240
DB 181 RNVSLPLEEERKSSYQLQVRAAPQGTISFRGTSEWSDPYIFOTQAEPEAGNDPHLL 240
QY 241 LLLLVIFIPAFWMLKTHPLRLMKIWA--VSPERFPMPLKXGSGDFKXKVGAPFGS 299
DB 241 LLLLVIFIPAFWMLKTHPLRLMKIWA--VSPERFPMPLKXGSGDFKXKVGAPFGS 299
QY 300 SLELGPMSPVSTLEVYSCHPSPRSYAKRLQTLQEPALVESDGVKPSFW--PTAQ 356
DB 300 SLELVPSSTTSLV-----HLSTLYPAKEXKFGPLGLEQLECDGMEPCGHWCITPLAA 354
QY 357 NSGSAATSEERDRYGLVSTITVYVLDAGECTWPCSEEDGYPALDDAGLESPGLSD 416
DB 357 NSGSAATSEERDRYGLVSTITVYVLDAGECTWPCSEEDGYPALDDAGLESPGLSD 416
QY 417 PLLDAGTIVTSCGCVSAGSPGLGSLDLRLKPLADGEDMAGLPMGGRSPGVSES 476
DB 415 LLLVTDPAFLSCGCVSAGSLRLGSPSLRLRLSPKEDGWTADPTWRTGSPGSGSES 474
QY 477 EAGSPPLAGLMDTDFDSGFGVSDCSSPVACDFTSPQDEGPPRSYLQWVVIPIPLSSPGPQ 536
DB 475 EAGSP-PGLMDTDFDSGFGVSDCSSPVACDFTSPQDEGPPRSYLQWVVIPIPLSSPGPQ 527
QY 537 AS 538
DB 528 SS 529

RESULT 5
QSEBBI_RAT PRELIMINARY; PRT; 521 AA.
AC QSEBBI;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DE 07-FEB-2006, entry version 9.
DE Interleukin 21 receptor (Predicted).
GN Name=IL21r;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Uebin T.B., Toshitsuki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
CC -!- DOMAIN: The WSKWS motif appears to be necessary for proper protein

CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC -----
CC EMBL, BC089857; AA089857.1; -; mRNA.
CC DR GO, GO:0016021; C:integral to membrane; IEA.
CC DR GO, GO:0004872; F:receptor activity; IEA.
CC DR InterPro, IPR003531; Hempr rcpt S Fl.
CC DR PROSITE, PS01355; HEMATOPOI_REC_5_F1; UNKNOWN_1.
CC KM Receptor, Transmembrane.
CC SQ SEQUENCE 521 AA; 57439 MW; 37DEF84AE58D759A CRC64;
Query Match 57.6%; Score 1703.5; DB 2; Length 521;
Best Local Similarity 63.3%; Pred. No. 3.7e-113;
Matches 341; Conservative 47; Mismatches 132; Indels 19; Gaps 7;
QY 1 MPRGAAPLLILLIIGGWCEDLVCTDYLCIEMKNIHSTLTITQDYBELKD 60
DB 1 MPRGLAAPLLILLIHGWSCLDLCYTDYLTITCIVLETWSPNPSILSTLTQDYBELKD 60
QY 61 EATCSLHRSANHTATYTCCHMDVPHPMADDFRSVNTTDSQGNYSOECGSLAESIKP 120
DB 61 KETSCSLHAGSHNTHTMHTCHMRLSQPMDSDDVFTVNMDDSSNSQECGSLAESIKP 120
QY 121 APPNVTVTSGQYNIISMRSDYEDPAFYMLKGLQYELQYRNRPDPAVSPRRKLISYDS 180
DB 121 APPLNVTVTSGRIDISMDSTIYEEPSNVYLRGKQYELQYRNRLDPAVAVRTKLISYDS 180
QY 181 RSVLLPLEFRKSSYELQVRAGMPGSSYOGTWSWSDPYIFOTQSEELKEGNPHLL 240
DB 181 RNISLLPQEFKSSYQLQVRAAPQGTISFRGTSEWSDPYIFOTQAEPEAGNDPH--VL 239
QY 241 LLLLVIFIPAFWMLKTHPLRLMKIWA--VSPERFPMPLKXGSGDFKXKVGAPFGS 299
DB 241 LLLLVIFIPAFWMLKTHPLRLMKIWA--VSPERFPMPLKXGSGDFKXKVGAPFGS 299
QY 240 LLLVLLIVLIVFMGLKHLPLRLCKKIWA--VSPERFPMPLKXGSGDFKXKVGAPFGS 299
DB 240 LLLVLLIVLIVFMGLKHLPLRLCKKIWA--VSPERFPMPLKXGSGDFKXKVGAPFGS 299
QY 300 SLELGPMSPVSTLEVYSCHPSPRSYAKRLQTLQEPALVESDGVKPSFWPTAQNSG 359
DB 300 SLELGPMSPVSTLEVYSCHPSPRSYAKRLQTLQEPALVESDGVKPSFWPTAQNSG 359
QY 357 NSGSAATSEERDRYGLVSTITVYVLDAGECTWPCSEEDGYPALDDAGLESPGLSD 416
DB 357 NSGSAATSEERDRYGLVSTITVYVLDAGECTWPCSEEDGYPALDDAGLESPGLSD 416
QY 417 PLLDAGTIVTSCGCVSAGSPGLGSLDLRLKPLADGEDMAGLPMGGRSPGVSES 476
DB 415 LLLVTDPAFLSCGCVSAGSLRLGSPSLRLRLSPKEDGWTADPTWRTGSPGSGSES 474
QY 477 EAGSPPLAGLMDTDFDSGFGVSDCSSPVACDFTSPQDEGPPRSYLQWVVIPIPLSSPGPQ 536
DB 475 EAGSP-PGLMDTDFDSGFGVSDCSSPVACDFTSPQDEGPPRSYLQWVVIPIPLSSPGPQ 527
QY 537 AS 538
DB 528 SS 529

RESULT 6
Q3TA82_MOUSE PRELIMINARY; PRT; 292 AA.
AC Q3TA82;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DE 07-FEB-2006, entry version 5.
DE Activated spleen cDNA, RIKEN full-length enriched library,
DE clone:FB830031M06 product:interleukin 21 receptor, full insert
DE sequence. (Fragment).
GN Name=IL21r;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

- [1]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=Activated spleen;
RA MEDLINE=9927925; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Methods Enzymol. 303:19-44(1999).
[2]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=Activated spleen;
RA PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells S., Kodius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.P., Wilting L.G., Aidinis V., Allen J.E., Bailey T.L.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Guclincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Keiso K., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Ljung S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottacuda H., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schombach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takanaka Y., Taki K.,
RA Tammojä K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zdobych E., Zhu S., Zimmer A., Hilde W., Bolt C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawaguchi N.,
RA Kawahara T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome";
RL Science 309:1559-1563(2005).
[3]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=Activated spleen;
RA PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense transcription in the Mammalian Transcriptome";
RL Science 309:1564-1566(2005).
[4]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=Activated spleen;
RA MEDLINE=2235683; PubMed=1246685; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nakajima I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bolt C., Hume D.A., Quackenbush J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bratt D., Brusic V., Chochis C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Guclincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perla G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelain A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilting L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavanon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirokawa N., Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Haashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
[5]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=Activated spleen;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Waehnle T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bolt C., Fletcher C., Fujita M., Gariboldi M.,
RA Guclincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli U., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
[6]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=Activated spleen;
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
[7]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=Activated spleen;
RA MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed sequencer";
RL Genome Res. 10:1757-1771(2000).
[8]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=ND; TISSUE=Activated spleen;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kangawa S.,
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watabiki A.,

RL Genome Biol. 6:R6-R6(2005).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (By similarity).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 CC EMBL, AJ851394; CA65028.1; -; mRNA.
 DR GO: GO:0016021; C: integral to membrane, IEA.
 DR InterPro: IPR007110; IG-like.
 DR PROSITE, PS50835; IG_LIKE; 1.
 KM Hypothetical protein; Immunoglobulin domain; Repeat; Transmembrane.
 SQ SEQUENCE 590 AA; 66332 MW; 369CA0869A5867 CRC64;
 Query Match 25.8%; Score 764; DB 2; Length 590;
 Best Local Similarity 33.0%; Pred. No. 6.5e-46;
 Matches 193; Conservative 88; Mismatches 210; Indels 94; Gaps 19;
 QY 12 LLLGGGCGCDLVYTDYVLTQVVICILEM-WMLHPSTLTLMQDQYELKDEATCSLHRS 70
 DB 14 LLEFYSTCHENTLTFVDYVDTLSTCLRNLDGASPYNITATWDE-DDPENIVAACSLLEL 72
 QY 71 AHNATHATYTCMDVFHFMDIFSVNITDQSGNYSOEGCSFLLAESIKRAPPNVTVT 130
 DB 73 SRNANHTEYCTVDMTELADIRVQVDATEIADRHVYISIGFYKKDNIRPQPFNLTAVF 132
 QY 131 SGQYNIWSRDEYEDPAFYMLKGLQYELQYRNQDPMNAVSRKLISVDSKVSLLPLEF 190
 DB 133 TEGYNIMETHTQHPFLFYLLNGELEQYLRKRRADTWE-TOKIKSVEDKKTAVILPQEF 191
 QY 191 RKXSSVLEIYRAGMPSSVQGTWSESDPRTFQTSSELEK-----GWNPHLLLLLV 246
 DB 192 QGNTVEFYQVARRGGTGYGFGEWSSRLTLTSPAAVYQRAQMGW-----MLFVVA 246
 QY 247 VFIPAFSLKTHPLMLMKKIWAVSPERFMPPLKYGSGDFFKKVGAFTGSSLELGPW 306
 DB 247 MVTASTATPLAKQSLMKKIACIPDSAPFKPLIYMWNGFFKMWGSHMKMTIDLFEW 306
 QY 307 SPEVPSLTLEYVSCPPRSPAKRLQLTQLQEPALVESDGVKPSF---WPTAQN--SGG 360
 DB 307 EIVPSEVLEVFMSRPSNCTG-----QEEIRLEKNDLPCKPCVSGILTFVQDSSLISV 358
 QY 361 SAYSEEDRPYGLVSIQTVTVTLDAEGPCTWPCSC-----EDDGYPALDL 404
 DB 359 NSSSVTPDRSYGHLSIDITVYADFTPCNCCQCNRMKYKQKNGDEDSAESESTPKVNI 418
 QY 405 -DAGLEPSPGLEDELDTAGTIVLSGCGVS-----AGSPG-----LGGPLGSLDR-- 448
 DB 419 DDEBRRRSSALHLSLDSQDKILASGSMSTHLLRTTGAPGHQKVEGALLEGMSILAEFC 478
 QY 449 LKP-----PLADGE--DMAGG---LPMGGRSPGVSESEAGSPLAGIDMTFD 491
 DB 479 LHPQMDLENPASLPSPDGESVSESGCDFPFRGAR-PGG-----SYMICIDLDTID 531
 QY 492 SGFVSGDCSSPVEDCFITSPGD-----EGPSPSYLRQWV 524
 DB 532 SGFVSDSGSPVDFEFGNSQTNASVPLBOEGEDFPKSYVKQNI 576
 RESULT 9
 IL2RB_MACFA
 ID IL2RB_MACFA STANDARD; PRT; 551 AA.
 AC Q38J85;
 DT 23-JAN-2006, integrated into UniProtKB/Swiss-Prot.
 DT 22-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
 DE (High affinity IL-2 receptor beta subunit) (CD122 antigen).
 GN Name=IL2RB;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.

OX NCBI_TaxId=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RA Chen S., Yu L.
 RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for Interleukin-2. This beta subunit is
 CC involved in receptor mediated endocytosis and transduces the
 CC mitogenic signals of IL2 (By similarity).
 CC -1- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
 CC exists in 3 different forms: a high affinity dimer, an
 CC intermediate affinity monomer (beta chain), and a low affinity
 CC monomer (alpha chain). The high and intermediate affinity forms
 CC also associate with a gamma chain (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (By similarity).
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intercellular transport and cell-
 CC surface receptor binding (By similarity).
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
 CC activation (By similarity).
 CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4
 CC subfamily.
 CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
 CC -----
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 CC -----
 CC EMBL, DQ223724; AB003908.1; -; mRNA.
 DR PROSITE, PS50853; FN3; 1.
 DR PROSITE, PS01355; HEMATOPOIETIN_R, 1.
 KM Glycoprotein; Membrane; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 26
 FT CHAIN 27 551
 FT TOPO_DOM 27 240
 FT TRANSMEM 241 265
 FT TOPO_DOM 266 551
 FT DOMAIN 131 229
 FT MOTIF 220 224
 FT MOTIF 278 286
 FT CARBOHYD 29 29
 FT CARBOHYD 43 43
 FT CARBOHYD 71 71
 FT CARBOHYD 149 149
 FT DISULFID 36 46
 FT DISULFID 74 86
 SQ SEQUENCE 551 AA; 61224 MW; 5CEAECLA802A1050 CRC64;
 Query Match 9.9%; Score 294; DB 1; Length 551;
 Best Local Similarity 26.4%; Pred. No. 2.4e-12;
 Matches 139; Conservative 73; Mismatches 200; Indels 114; Gaps 30;
 QY 5 WAAPLLILLLLGGW-----GCPDLVCTDYLTQVVICILEMNHPSLTTLTWQDYE 56
 DB 8 WCLPLILLILLPLATSSASAANVTGSRFTCFYNSRANISCV---WS-----QDG 52
 QY 57 ELKDEATSCSLH---RSANNAI-----HATYTCM-----DVHFEMADIFSVNITD 100
 DB 53 ALQD--TSCVNHAMPDRRRNQTCELLPVSOAMWACLILIGTDPDQKLTAVDITLTKVMC 110
 QY 101 QSGN--YSQEGSFLLAESIKRAPPNVTVT--SGQYNIWSRDEYEDPAFYMLKGLQY 156
 DB 111 REGVRRMMALIQPKPPENIRLMAPISTQVYVHETRCNSMKT---SQASHFEERLEF 167
 QY 157 ELQYRNQDPMNAVSRKLISVDSKVSLLPLEFRKDSYEIQVRAGPMFGSSYQGTWSE 216
 DB 168 EARTLPSGHTWEAP---LMTTLKQKQEWICLETFLPTDQYEFQVRYVPLQGEF--TTWSP 222
 QY 217 WSDPVLFTQTSSELEKSG--WNPPLLILLLVVVFIPAFNSL---KTHPLMLW--KKIW 268
 DB 223 WSPPLAFRTPALGKDTIPLGLHLVGLSGAFIILVYLLINCRNTG---WLKKVL 278
 QY 269 A--VSPERFMPPLKYGSGDFFKKVGAFTGSSLELGPWSPVPSTLLEYVSCPPRSPA 326

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Db      279 KCHTPBPSKFFSQTLSHGSDVOKMLSSFPSSSFSGGLAPRI-SLEY-----L 328
Qy      327 KRLQTELOBPALVESDGVPKPSFWPTAONSGSAYSEERDPYGLVSDITVTLDAEG 386
Db      329 ERKVTQL-----LLOQDKVPEPS-----SLSSNRLTSCFTNOGYFFPHLPDALEIA-- 377
Qy      387 PC-----TW-PCSGEDDGYPLALDAGLEPSP-----GLEPDLDACTVLSGCCVSAAGSP 437
Db      378 -CQVYFTYDPCABEEDEGADAPTGSSPQPLRLSAED---DAYCTFPGDDLLEFSPS 433
Qy      438 -LGGP-----LGLDLRLKPLAD--GEPMAGGLPMGGRSPG 471
Db      434 LGGPSPPTAPEGSGAGEERLPSLQGERVPRDM-DPQLGPRTPG 478

RESULT 10
06UAP3_TETNG
ID 06UAP3_TETNG PRELIMINARY; PRT; 512 AA.
AC 06UAP3;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE Class I helical cytokine receptor member 13.
GN Name=CRFAL3;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphia; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontinae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mancel E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossaet C., Segurens B.,
RA Desliva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Kallinka M., Vacherie B.,
RA Blomont C., Skalli Z., Castejolo L., Poulain J., De Bernardinis V.,
RA Cruaud C., Dupret S., Broctier P., Couanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chappe R., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolf J.-N., Guilo R., Zody M.C., Westrov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RA "genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
CC -----
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CC -----
DR EMBL: AY374485; AAR25676.1; -, mRNA.
DR Ensemble: AY374485; Tetraodon nigroviridis.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PSS0653; FN3; 1.
KM Receptor.
SQ SEQUENCE 512 AA; 57191 MW; E058418483A5DF0B CRC64;

Query March 9.7%; Score 286; DB 2; Length 512;
Best Local Similarity 24.4%; Pred. No. 8,1e-12;
Matches 143; Conservative 76; Mismatches 203; Indels 164; Gaps 29;
Qy 10 LLLLLGGGMCPCDLY-----CYTDYLGTVTC-ILEMKNLHPSLTTLTMOQVYELKDEA 62
Db 14 LLLLVQ-----CAAVVSRGNVTCSTDYNNVSLNCSGCAEAVQTRSVFLHVKCSDEGDIVD-- 67
Qy 63 TSCSLHSAHNATATYTCCHMDVHFMA-----DQIFSVN-----ITQSGN--YSQ 107
Db 68 -----SCEVKEPQSWCWSPESLIEDLVSTWICDARATGDAPIDSS 110

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Qy 108 ECGSFLAASIKPAPENVTVT-FSGQYNISW-RSDYEDPAFYMLKQLQYELQYNNRGD 165
Db 111 EEPSSMLCDVAVKEPASA RVTNTEDSYNTVTHVNVQDLCTIVAR-----VRENRR-- 162
Qy 166 PNAVSRRKLIISDSSVSLPLEFRKSSYELQVRAGEMPSSYQGTWSEWDVY-IFQ 224
Db 163 -MSKEVYSVL-SDSGHLDIISELLQPRVGYLDVAVAKKCPGLYEGPWSSEWSSAIEIRP 220
Qy 225 TQSEELKEGNHLL-----LLLLVYVFIPAFWSLKTPLRMKIKIAVPSPEEFMP 279
Db 221 AATSDIAMSQ--HLFYTPSVLTLVVVSVLSYLLKNH-----QIPREHFPAV 268
Qy 280 LYKSGSGDFPKWGAFF-----TGSSL-----ELGWPSPVPSTLEVYSGHPRSPA 326
Db 269 LHNNGDFFKEMVNPVFKCEDYIMTSGVQVMKQEDLLQWNSKESSTESKNNKHGHF 328
Qy 327 KRLQTELOBPALVESDGVPKPSFWPTAONSGSAYSEERDPYGLVSDITVTLDAE- 385
Db 329 PKLQAO--AHPILLGSDWG-----SQSRGLA-----QPSIHVTLSSEEE 368
Qy 386 -----GPTWPCSGEDDGYPLALDAGLEPSPGLEDPDLDACTVLSGCCVSAAGSP 436
Db 369 FEEEGTSQSSACVLRSDODRESFEVEEDWKEQAAGLEB-----AASGLP 414
Qy 437 GLGGLPLSLDLRLKPLADGEDMAGGLPMGGRSPGVS-----ESEAGSPLAGLMD 488
Db 415 -----PVLQORASSSSGSEDDVLPHPQFFAEKRVSLDSLANDQSEGYIP--HYDLD 465
Qy 489 TFDSGFVSGDSSPVBCDFTSPGDEGPP-----RSYLROWV 525
Db 466 TIDSGF--GEYNSP-----GASPGADQTSLHEINLHNSVYKQMW 505

RESULT 11
IL2RB_PANTR
ID IL2RB_PANTR STANDARD; PRT; 551 AA.
AC Q38084;
DT 10-JAN-2006, integrated into UniProtKB/Swiss-Prot.
DT 22-NOV-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Interleukin-2 receptor beta chain precursor (IL-2 receptor) (P70-75)
DE Interleukin-2 receptor beta chain subunit (CD122 antigen).
DE (High affinity IL-2 receptor beta subunit) (CD122 antigen).
GN Name=IL2RB;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RA Chen S., Yu L.;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for interleukin-2. This beta subunit is
CC involved in receptor mediated endocytosis and transduces the
CC mitogenic signals of IL2 (By similarity).
CC -1- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
CC exists in 3 different forms: a high affinity dimer, a low affinity
CC intermediate affinity monomer (beta chain), and a low affinity
CC monomer (alpha chain). The high and intermediate affinity forms
CC also associate with a gamma chain (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane, single-pass type I membrane
CC protein (By similarity).
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4
CC subfamily.
CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
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CC EMBL: DQ23725; ABB03909.1; -- mRNA.

DR PROSITE; PS50853; FN3, 1.

DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.

KW Glycoprotein; Membrane; Receptor; Signal; Transmembrane.

FT SIGNAL 1 26 By similarity.

FT CHAIN 27 551 Interleukin-2 receptor beta chain.

FT 1 /Ftrd=PRO_0000045410.

FT TOPO_DOM 27 240 Extracellular (Potential).

FT TRANSHEM 241 265 Potential.

FT TOPO_DOM 266 551 Cytoplasmic (Potential).

FT DOMAIN 131 229 Fibronectin type-III.

FT MOTIF 220 224 WSXWS motif.

FT MOTIF 278 286 Box 1 motif.

FT CARBOHYD 29 29 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 43 43 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 71 71 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 149 149 N-linked (GlcNAc. . .) (Potential).

FT DISULFID 36 46 By similarity.

FT DISULFID 74 86 By similarity.

SO SEQUENCE 551 AA; 61126 MW; 5C4B1CB17BEF52B CRC64;

Query Match 9.5%; Score 280; DB 1; Length 551;

Best Local Similarity 25.6%; Pred. No. 2,4e-11;

Matches 134; Conservative 76; Mismatches 204; Indels 110; Gaps 30;

5 WAAPLLILL--LQCG-----GCPDVCYTDYDQYICLEMNHLPTLTWQOYE 56

8 WRPLPLLLPLATPMASATVNGTSOPTCYNSRANISCV-----WS-----ODG 52

57 ELDEATSGSLH-----RSANNA-----HATYCHM-----DVHFMAADIFSNITD 100

53 ALQD--TSCVHAMPRDIRRNNQTELLPVQSASACNLIIGAPSOGLTDTITLKYLC 110

101 QSGNYSOECG--SFLLAESIKPAPFPVNTYTF--SGQYNISWSDYEDPAFYMLKGLQY 156

111 REGVNRVMAIQDKFPENRLMAPISLQVHVETHRCNISMEI---SQASHYERHLIEF 167

157 ELQVRNKGDMWASPPRKLSVDSRSVSLPLERKSSSYELQVRAGPMSSYQGTWSE 216

168 EARTLSFGHTWBEAP--LTLTKQKQEWICLETLPPTQYEFQVRYKPLQGEF--TTWSP 222

217 WSPVIRFQTOSEBEKEG--WNPHLLLLLVIFAFAPMSL-----KTHPLRLM--KKIW 268

223 WSOPLAFRTKPAISGKOTTPMLGHLVGLSCAFPIILVILIKCRNTGP---WLKKVL 278

269 A--VPSPERFEMPLYKCGSGDFKKMGVAPFTGSSLELGPMSPVSTLEVYSCHPRSSPA 326

279 KCHTPDSKFFFSQLSSEHGQVQKWLSPFSSSFSGGLAPEI--SPLEV-----L 328

327 KRLQLETPALPABELVEDGVPKPSFWPTAQNSSGASVSEEDRYGLVSDITVVDLAE 386

329 ERDKVTOL-----LLQDDKVPBP-----SLSSNHSLSCTFNQGYFFPHLPDALEIEA-- 377

387 PC-----TWPCSCEDD-----GYPALDLADGLEPSPGLD-----PLLDAGTVLSCGV 431

378 -COVFTYDPAEEDDAEGVAGAPRTGSSPOLPLQSGEDDYCTFPSSRD--GLLIFPSLL 435

432 SAGSPGLGPGLSLL--DRLKPLAD--GEDMAGLPMGGRSPG 471

436 GGPSPSTAPGSGAGEERMPSPSQERVPRDW--DPOPLGPTPG 478

GN Name=IL2RB;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=89242117; PubMed=2785715;

RA Hakeyama M., Tando M., Minamoto S., Kono T., Doi T., Miyata T.,

RA Miyasaka M., Taniguchi T.,

RT "Interleukin-2 receptor beta chain gene: generation of three receptor

RL forms by cloned human alpha and beta chain cDNA's,"

RL Science 244:551-556(1989).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RX PubMed=15461802; DOI=10.1186/gb-2004-5-10-r84;

RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,

RA Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle E.J.,

RA Beare D.M., Dunham I.,

RT "A genome annotation-driven approach to cloning the human ORFeome,"

RL Genome Biol. 5:RESEARCH84.1-RESEARCH84.11(2004).

RN [3]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RA Rieder M.J., Amel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,

RA Rajkumar N., Toth B.J., Yi Q., Nickerson D.A.;

RT "SeatleSNPs, NHLBI H66682 program for genomic applications, UW-

RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>)";

RL Submitted (JUN-2002) to the EMBL/GenBank/DBD databases.

RN [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,

RA Clamp M., Smink L.J., Alincough R., Almeida J.P., Babbage A.K.,

RA Beguney C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Bugees J.,

RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,

RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,

RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,

RA Gilbert J.G.R., Goward M.E., Grafton D.V., Griffiths M.N.D., Hall C.,

RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,

RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,

RA McElay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,

RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.D.C.T.,

RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,

RA Scott C.E., Senra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,

RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers S., Shimizu N.,

RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudo Y.,

RA Shirotsuki A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuuya S.,

RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,

RA Lewis J., Lewis S., Lin S.-P., Lon P., Mala J.E., Nguyen T., Pan H.,

RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,

RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,

RA Zhan M., Zhang G., Chisese S., Murray J., Miller N., Mlax P.,

RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,

RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,

RA Hinds K., Kemp K., Lareille P., Layman D., Ozerky P., Rohlfing T.,

RA Scheet P., Walker C., Wamley A., Wohldmann P., Pepin K., Nelson J.,

RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,

RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salta S.,

RA Bedarf M.L., Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,

RA Edelmann L., Kim U.J., Shizuya A., Simon M.I., Dumanecki J.P.,

RA Peyrard M., Kedra D., Serousi E., Franson I., Tapia I., Bruder C.E.,

RA O'Brien K.P., Wilkinson P., Bodentelch A., Hartman K., Hu X.,

RA Khan A.S., Lane L., Tlahun Y., Wright H.;

RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pakey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhe U.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP 3D-STRUCTURE MODELING OF 31-230.
RX MEDLINE=9511955; PubMed=7529123;
RA Bamotrough P., Hedgecock C.J., Richards W.G.;
RT "The interleukin-2 and interleukin-4 receptors studied by molecular
modelling.";
RT Structure 2:839-851(1994).
CC -1- FUNCTION: Receptor for interleukin-2. This beta subunit is
involved in receptor mediated endocytosis and transduces the
mitogenic signals of IL2.
CC -1- SUBUNIT: Noncovalent dimer of an alpha and a beta chains. IL2R
exists in 3 different forms: a high affinity dimer, an
intermediate affinity monomer (beta chain), and a low affinity
monomer (alpha chain). The high and intermediate affinity forms
also associate with a gamma chain.
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
protein.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
folding and thereby efficient intracellular transport and cell-
surface receptor binding.
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
activation.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 4
subfamily.
CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
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CC -----
DR EMBL; M26062; AAA59143.1; -; mRNA.
DR EMBL; CR456506; CAG30392.1; -; mRNA.
DR EMBL; AF517934; AAM54040.1; -; Genomic DNA.
DR EMBL; AL022314; CA18444.1; -; Genomic DNA.
DR EMBL; BC025691; AA25691.1; -; mRNA.
DR FIR; A30342; A30342.
DR PDB; 1ILM; Model; B=31-230.
DR PDB; 1ILN; Model; B=31-230.
DR PDB; 2BS1; X-ray; B=27-240.
DR Ensembl; ENSG00000100385; Homo sapiens.
DR H-InvDB; HIX0016437; -.
DR HGNC; HGNC:6009; IL2RB.
DR MIM; 146710; gene.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0004911; F:interleukin-2 receptor activity; TAS.
DR GO; GO:0006461; P:protein complex assembly; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR002996; Cytokn rcptl_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003531; Hempe_rcptl_S_F1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS50853; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW 3D-structure; Glycoprotein; Membrane; Polymorphism; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 26
FT CHAIN 27 551
FT
FT TOPO_DOM 27 240
FT TRANSMEM 241 265
FT TOPO_DOM 266 551
FT DOMAIN 131 229
FT MOTIF 220 224
FT MOTIF 278 286
FT CARBOHYD 29 29
FT CARBOHYD 43 43
FT CARBOHYD 71 71
FT CARBOHYD 149 149
FT DISULFID 36 46
FT DISULFID 74 86
FT VARIANT 83 83
FT VARIANT 83 83
FT VARIANT 391 391
FT STRAND 35 37
FT STRAND 39 43
FT STRAND 45 47
FT STRAND 51 57
FT STRAND 60 64
FT STRAND 66 67
FT STRAND 68 70
FT STRAND 72 73
FT STRAND 75 76
FT TURN 80 82
FT STRAND 85 86
FT TURN 90 92
FT HELIX 93 95
FT STRAND 96 104
FT STRAND 106 109
FT STRAND 112 116
FT STRAND 118 122
FT STRAND 132 133
FT STRAND 138 138
FT HELIX 139 142
Query Match 9.4%; Score 278; DB 1; Length 551;
Best Local Similarity 26.0%; Pred. No. 3.3e-11;
Matches 137; Conservative 75; Mismatches 199; Indels 116; Gaps 31;
QY 5 MAAPLILLL--LGGW-----GCPDLVCYTDVLYQYICLLEMMNHLPTLTLTWQOYE 56
DB 8 WRPLPLLLPLPLTSMASAAVNGTSQTCFYNSRANISCV--WS-----ODG 52
QY 57 ELKDEATSCSIH-----RSANAT-----HATVTCM-----DVFHMAADIFSVNITD 100
DB 53 ALQD--TSCQVHAMPPDRRNRNQCCELLPVSQAQACNLIGAPDSOKLTTVDITLRLVLC 110
QY 101 QSGNYSOECG--SFLAESTIKPAPPFNVYTF--SGQYINISMSDVEDPFPYMLKGLQY 156
DB 111 REGVWRVMAIOQFKPFENIRLMAPISTQVHVHETHRCNISTWEI--SQASHYFERHLF 167
QY 157 ELQRRNRGDPWAVSPRRKLISVDSRSVSLPLEFRKDSYELQVRAGPMGSSYQGTWSE 216
DB 168 EARTLSFGHTWEAP--LITLKQKQEWICLETUTLPDTQYEFQVRKPLDGER--TWSP 222
QY 217 WSDPVIFOTOSSEIKKEG--WNPHLLLLLVIVFIPAFMSL-----KTHPLMLRW-KKIW 268
DB 223 WSGPLAFRTKPALAKQOTIWMGLHLVLGSGARGFILLVYLLINCRVTGP-----MLKVL 278
QY 269 A--VPSERFRFMPLYKCGSDPFKKWGVAPFTGSSLELGMSPSPVPSLTLEYSCHPNPSA 326

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Db 329 ERDKVETOL-----LLQDQKVEPEA-----SLSSNSHLTSCFTNOGYFFPHLLDALEIEA-- 377
Qy 387 PC-----TPWPCSCED-----GYPALDLADLEPSGLEPDLADGTTVLSGCVASGSP 436
Db 378 -CQVYFTYDYSEDPDEGVAAGAPTGSSPQLPLSG-ED--DNYCTFPRDILLFSP 432
Qy 437 G-LGGP-----LGLSLDLRLKPLAD--GEDMAGGLPWGGRSPG 471
Db 433 SLUGPSPSPSTAPGSGAGEERMPSLQERVRDWM-DPQLGPPPTPG 478

RESULT 13
Q2VB08 BRARE PRELIMINARY; PRT; 509 AA.
AC Q2VB08;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 4.
DE Erythropoietin receptor.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Paffett-Lugaassy N.N., Yang C., Paw B., Leschinsky I., Barut B.,
RA Bahary N., Caro J., Handin R., Zon L.,
RT "Functional conservation of epo-epr signaling in zebrafish.";
RL Submitted (NOV-2005) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -----
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CC
DR EMBL; DQ273166; AB877800.1; -, mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR KW Membrane; Receptor; Repeat; Transmembrane.
DR SQ SEQUENCE 509 AA; 57872 MW; ADA014E174FCD380 CRC64;

Query Match 8.8%; Score 261; DB 2; Length 509;
Best Local Similarity 26.5%; Pred. No. 4.9e-10;
Matches 130; Conservative 70; Mismatches 204; Indels 86; Gaps 25;

Qy 22 DLVCYTDYLTQVTCILEN--WNLHPSLTLYTWDQYELKDEATSGLSRSHANATHAT 78
Db 41 DIKCFVGGKQDFTCFWEKEDGTNSODNYFTTYMENKMDCAVS-SLFLSSN--RSV 97
Qy 79 YTCNM-DVFHFMADDISVNTTDSQNSQCSFLAESTKRAPPNVYTFP--GQY 134
Db 98 FPCCLPALFTSLDVOVLRDGQMLYKNSLVENILLTD-----PRAVYTWSSGKEGQL 152
Qy 135 NISWRSDYEDPAFMLKGLQYELQYRNRPDPAVSPRKLISVDSRSVSLPLE-PRKD 193
Db 153 NVSLNL-----PRAVYKIDSLIYEVY-----AVESHMCKVETKASTMLVLRGLQPD 201
Qy 194 SSYELQVRAGMPGSSYGQTSWSESDPYIFOTGSEBLEKGNPHLLILLIVIFIPAFW 253
Db 202 TRYKVMRVRKP-DGVSYKGYWSSWTSPVIAVT-----PGSMDBLIVLVLVFIILICLL 255
Qy 254 S-----LKTHTPLMRMKKTIWA-VPSPEPFMPLVYKCGSGDPFKWVGAPPTGS-----SLELG 304
Db 256 SMYVILSHHKF--LLKKLMPDIPTEHKFPGLFTVYKGFEXEM-SQNSGSMWARSVQM- 311
Qy 305 PMSPEVSTLEVYSCHPSPAPKRLQTLQELQPAELVESD-----GVKPSFMPPTAQNNG 359
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Db 312 -YTEELPSPLEVLS-----EVSLSPLDERKLVREDDQSDSGLTERRPHLMEOGLRA 361
Qy 360 GSATSEERDRPYGLVSTDT-VTVLDABGPTWCSCEDDGYPALDLADGLEPSPGLEPDL 418
Db 362 LQENPESLSSTLQSHDYITLHNSGG-----QREDDVF-----ETLPIQLTLF 407
Qy 419 LDAGTVLSCGCVASVAGPGIGPGLSLDLRLKPLADGEDMAGGLPWGGRSPGVSSSEA 478
Db 408 TSNQTSINNSHDLGLSLRQSSASGRLSQ-----SSEFD--PNHPMPRPGGYAVMAVA 460
Qy 479 GSPLAGLMD 488
Db 461 DS---GVSLD 467

RESULT 14
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AC Q9Z1A0;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Interleukin-5 receptor beta chain.
GN Name=IL5;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Logsdon N.J., Graham A., Scott C.W.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -----
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CC
DR EMBL; U94688; AAC77520.1; -, mRNA.
DR HSRP; P32927; IGH7.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004907; F:interleukin receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p. .; IEA.
DR InterPro; IPR002996; Cytln rcpt_B/C.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003531; Hempc_rcpt_S_F1.
DR InterPro; IPR011365; IL3_rcpt_beta.
DR Pfam; PF00041; fn3_3.
DR PIRSF; PIRSF001956; IL3R_beta_c_1.
DR SMART; SM00060; FN3; IL3.
DR PROSITE; PSS0853; FN3_3.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN 1.
DR KW Membrane; Receptor; Transmembrane.
DR SQ SEQUENCE 890 AA; 96579 MW; D43FB1CA852536 CRC64;

Query Match 8.5%; Score 250; DB 2; Length 890;
Best Local Similarity 22.7%; Pred. No. 6.2e-09;
Matches 150; Conservative 73; Mismatches 217; Indels 220; Gaps 36;

Qy 2 PRGMAAPLILLLLQGGGCP-DLVCTYTDYLTQVTCILEMNNLHPSLTLYTW----- 51
Db 229 PSMQSPVSVSSQPGDQAGQNLQCVFDAGHTLSCGMEVRSQVTSVSGFLFYRSSLDAG 288
Qy 52 -----QDQYELKDEAT--SCSLHRSANHNATHATYTCMDVFRHMADLIFSUNITDQSG- 103
Db 289 EQRCPQVQKELHLDIYTRHSCQI-RVSNPRPHSQYT-----VTVPRANGE 332
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Db      407 LPPLPFTGERDDYCAFPPRDILL-----FSPSMSTPNTAYGNSITPEER 452
QY      451 PPLADGEDWAGLPLWGRSPGVSESEAGSPLAGIDMDTFDSCFVGSDDCSSPVECDFTSP 510
Db      453 PPLSLQJ-----GLP-----SLASPDLMGL-----QHPLELEL--- 480
QY      511 GDEGPPRSYLRQWVVIPPPSSPGPOAS 538
Db      481 GDDEGMS-----TNSGQOAS 497

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Search completed: September 7, 2006, 12:51:27
 Job time : 300.669 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:51:46 ; Search time 53.8 Seconds
(without alignments)
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Title: US-10-659-684-115

Perfect score: 2958
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/iaa/5.COMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/iaa/6.COMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/iaa/7.COMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/iaa/H.COMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCUS.COMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/iaa/RC.COMB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/iaa/bbckfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2958	100.0	538	2	US-09-040-005-2
2	2958	100.0	538	2	US-09-522-217-115
3	2958	100.0	538	2	US-09-404-641-2
4	2958	100.0	538	2	US-09-923-246-115
5	2958	100.0	538	2	US-10-295-723-115
6	2958	100.0	538	2	US-10-414-186-2
7	2958	100.0	538	2	US-09-825-561A-2
8	2958	100.0	538	2	US-10-243-072-2
9	2958	100.0	538	2	US-10-282-622-16
10	2958	100.0	547	2	US-09-949-016-11544
11	2817	95.2	568	2	US-09-825-561A-65
12	1735.5	58.7	529	2	US-09-404-641-85
13	1735.5	58.7	529	2	US-10-414-186-85
14	1735.5	58.7	529	2	US-09-825-561A-12
15	1735.5	58.7	529	2	US-10-243-072-85
16	1729.5	58.5	529	2	US-09-734-234-6
17	1729.5	58.5	529	2	US-09-784-859-6
18	1302	44.0	567	2	US-09-825-561A-16
19	1231.5	41.3	397	2	US-09-404-641-81
20	1231.5	41.3	397	2	US-10-414-186-81
21	1231.5	41.3	397	2	US-10-243-072-81
22	1197	40.5	606	2	US-09-522-217-97
23	1197	40.5	606	2	US-09-404-641-51
24	1197	40.5	606	2	US-09-923-246-97
25	1197	40.5	606	2	US-10-295-723-97
26	1197	40.5	606	2	US-10-414-186-51

27	1197	40.5	606	2	US-09-825-561A-30	Sequence 30, Appl
28	1197	40.5	606	2	US-10-243-072-51	Sequence 51, Appl
29	1195	40.4	218	2	US-09-825-561A-6	Sequence 6, Appl
30	1135	38.4	261	2	US-09-825-561A-71	Sequence 71, Appl
31	1100	37.2	247	2	US-09-825-561A-69	Sequence 69, Appl
32	844	28.5	486	2	US-09-825-561A-73	Sequence 73, Appl
33	677.5	22.9	446	2	US-09-404-641-70	Sequence 70, Appl
34	677.5	22.9	240	2	US-10-414-186-70	Sequence 70, Appl
35	677.5	22.9	240	2	US-10-243-072-70	Sequence 70, Appl
36	278	9.4	551	2	US-09-194-145-2	Sequence 2, Appl
37	278	9.4	551	2	US-09-949-002-308	Sequence 308, App
38	278	9.4	551	7	5198359-2	Sequence No. 5198359
39	278	9.4	551	7	5449756-2	Sequence No. 5449756
40	278	9.4	594	2	US-09-949-002-537	Sequence 537, App
41	248.5	8.4	539	7	5449756-4	Sequence No. 5449756
42	247.5	8.4	539	7	5198359-4	Sequence No. 5198359
43	231	7.8	536	2	US-09-949-016-8560	Sequence 8560, Ap
44	220.5	7.5	468	1	US-08-164-614A-7	Sequence 7, Appl
45	220.5	7.5	468	1	US-08-456-489B-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-040-005-2
Sequence 2, Application US/09040005
Patent No. 6057128

GENERAL INFORMATION:

APPLICANT: Donaldson, Debra

TITLE OF INVENTION: MU-1 RECEPTOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/040, 005

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15320

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-498-8224

TELEFAX: 617-876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 538 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-040-005-2

Query Match

Best Local Similarity 100.0%; Pred. No. 3 6e-267; Indels 0;

Matches 538; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MPRGMAAPLILLLILQGSGCPDLVCYTDYICILEMNLAPSTLTLTQDQYEEIKD 60

Db 1 MPRGMAAPLILLLILQGSGCPDLVCYTDYICILEMNLAPSTLTLTQDQYEEIKD 60

QY	6	EATQSLRHSANAHATYTCAMDVFHMAADIFSNITDOSGNYQOEGSFLAASIKR	120
Db	61	EATQSLRHSANAHATYTCAMDVFHMAADIFSNITDOSGNYQOEGSFLAASIKR	120
QY	121	APPFVNTVTFSGQYNIWNRSDYEDPAFYMLKGLQYELQYRNKGDEMAVSPRKLISYDS	180
Db	121	APPFVNTVTFSGQYNIWNRSDYEDPAFYMLKGLQYELQYRNKGDEMAVSPRKLISYDS	180
QY	181	RSVSLLPLEFRDSSYLEQVAPGMPGSSYOGTWSMSDPVIFQTQSEELKEGWNHLL	240
Db	181	RSVSLLPLEFRDSSYLEQVAPGMPGSSYOGTWSMSDPVIFQTQSEELKEGWNHLL	240
QY	241	LLLLLIVEIIPAFWSLKTPLMLRMKIKIIVAPSPERFEMPLYYKCSGDFFKMYGAPFTGSS	300
Db	241	LLLLLIVEIIPAFWSLKTPLMLRMKIKIIVAPSPERFEMPLYYKCSGDFFKMYGAPFTGSS	300
QY	301	LELGWSPSEVBSTLEVYSGHPRRSPAKRIQLTELQEPALVBSBQVYKCSFWFTAQNSG	360
Db	301	LELGWSPSEVBSTLEVYSGHPRRSPAKRIQLTELQEPALVBSBQVYKCSFWFTAQNSG	360
QY	361	SAYSEERRPVGLVSDITVTYVLDABEPCWPCSCBEDGYPALDLNGLBPSPLAEPLLD	420
Db	361	SAYSEERRPVGLVSDITVTYVLDABEPCWPCSCBEDGYPALDLNGLBPSPLAEPLLD	420
QY	421	AGTTVLSGCVSAGSPGLGGLPLGLSLDLRLKPLADGEDWAGGLPMWGRSPGVYSEBAGS	480
Db	421	AGTTVLSGCVSAGSPGLGGLPLGLSLDLRLKPLADGEDWAGGLPMWGRSPGVYSEBAGS	480
QY	481	PLAGIDMTPTPSGPFVSGDCSSPVECDFTSPGDBGPRSLTRQWVYLPPLSLSPQDAS	538
Db	481	PLAGIDMTPTPSGPFVSGDCSSPVECDFTSPGDBGPRSLTRQWVYLPPLSLSPQDAS	538

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RESULT 522-217-115
US-09-522-217-115
Sequence 115, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 630702ak, Julia E.
APPLICANT: Premeel, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-09-522-217-115

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Query Match	100.0%;	Score 2958;	DB 2;	Length 538;
Best Local Similarity	100.0%;	Pred. No. 3.6e-267;		
Matches 538;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Oy 1 MPRGAAPLLLLLLLOGSMGCRPLVCYTDYLCQVACILEMKNLHPSTLTTLTWODQYBELKD 600
    |||||
Db 1 MPRGAAPLLLLLLLOGSMGCRPLVCYTDYLCQVACILEMKNLHPSTLTTLTWODQYBELKD 600

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Qy	61	EATSCGLHSSAHNAHTAATYTCMDVFEHMADIFSVNITTDQSNVSOECSCFLAEBIKP	120
Dp	61	EATSCGLHSSAHNAHTAATYTCMDVFEHMADIFSVNITTDQSNVSOECSCFLAEBIKP	120
Qy	121	APPFNVTVPSCQYNISMRSDYEDBAFYMLKGKQLQYELQYRNKRD PMAVSPRRKLISVDS	180
Dp	121	APPFNVTVPSCQYNISMRSDYEDBAFYMLKGKQLQYELQYRNKRD PMAVSPRRKLISVDS	180
Qy	181	RSVSLLPLEFRDSSYELQVRAGPMPGSSYOGTMSWMDPVIPOTOSBELKEGNPHULL	240
Dp	181	RSVSLLPLEFRDSSYELQVRAGPMPGSSYOGTMSWMDPVIPOTOSBELKEGNPHULL	240
Qy	241	LLLLVIVFIPAEFWSLKTHPMLRMKMKKIIVAVSPERFEMPLKYGCSGFKKWVGAPFTGSS	300
Dp	241	LLLLVIVFIPAEFWSLKTHPMLRMKMKKIIVAVSPERFEMPLKYGCSGFKKWVGAPFTGSS	300
Qy	301	LEIGPMSPEVPSTLEVYSCHPRPSPAKKLOLTLEOEPALVESNGVFKPSWMPAQNSSCG	360
Dp	301	LEIGPMSPEVPSTLEVYSCHPRPSPAKKLOLTLEOEPALVESNGVFKPSWMPAQNSSCG	360
Qy	361	SAYSESRDRPYGVASIDITYVLADAGPCMPWPCSCBDDCYPALDDAGLEPSPGLEDDPLD	420
Dp	361	SAYSESRDRPYGVASIDITYVLADAGPCMPWPCSCBDDCYPALDDAGLEPSPGLEDDPLD	420
Qy	421	AGTTVLSGCVSAGSPGLGGLGSLLDRLKPEPLADGEDWAGGLPMGGRSPGCVSEBAGS	480
Dp	421	AGTTVLSGCVSAGSPGLGGLGSLLDRLKPEPLADGEDWAGGLPMGGRSPGCVSEBAGS	480
Qy	481	PLAGLMDMPFDGFGVSCDSSPVEDDFPSPDEGPPRSYLRQWVITPPPLSSPPQAS	538
Dp	481	PLAGLMDMPFDGFGVSCDSSPVEDDFPSPDEGPPRSYLRQWVITPPPLSSPPQAS	538

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1  RESULT 3
2  US-09-404-641-2
3  Sequence 2, Application US/09404641
4  Patent No. 6576744
5  GENERAL INFORMATION:
6  APPLICANT: Presnell, Scott R.
7  APPLICANT: Conkell, Darrell C.
8  APPLICANT: No. 6576744ak, Julia E.
9  APPLICANT: Hammond, Angela K.
10 TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPPHALL1
11 FILE REFERENCE: 98-55
12 CURRENT APPLICATION NUMBER: US/09/404,641
13 CURRENT FILING DATE: 1999-09-23
14 PRIOR APPLICATION NUMBER: US 60/100,896
15 PRIOR FILING DATE: 1998-09-23
16 PRIOR APPLICATION NUMBER: US 60/123,546
17 PRIOR FILING DATE: 1999-03-09
18 PRIOR APPLICATION NUMBER: US 60/142,574
19 PRIOR FILING DATE: 1999-07-06
20 NUMBER OF SEQ ID NOS: 91
21 SOFTWARE: FastSeq for Windows Version 3.0
22 SEQ ID NO 2
23 LENGTH: 538
24 TYPE: prt
25 ORGANISM: Homo sapiens
26 US-09-404-641-2

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Query Match	100.0%;	Score 2958;	DB 2;	Length 538;
Best Local Similarity	100.0%;	Pred. No. 3.6e-267;		
Matches 538;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

1 MPRGMAAPLLLLLGGGCGCPDLVCTDYICIVICILEMNNLHPSTILTWTWQDQYEELKD 60

Oy 61 EATSCSLHRSAHNAHTATTCTCHMDVFHPMADIFSVNITDQSGNSQECCGFLAESTIKP 120
Db 61 EATSCSLHRSAHNAHTATTCTCHMDVFHPMADIFSVNITDQSGNSQECCGFLAESTIKP 120

Qy	121	PPFVNVYTFSSQYVNSIMSDYEDPAFYWLKGLQYELQYRNRGDPAWASPRKLLSVDS	180
Db	121	APPFNVYTFSSQYVNSIMSDYEDPAFYWLKGLQYELQYRNRGDPAWASPRKLLSVDS	180
Qy	181	RSVSLPLLEFRKDSSEYELQVRAQPMFGSSYQGTWSEMSDPVIFQTSSEELKEGMNPHLL	240
Db	181	RSVSLPLLEFRKDSSEYELQVRAQPMFGSSYQGTWSEMSDPVIFQTSSEELKEGMNPHLL	240
Qy	241	LLLLVIVFIPAAWMSLKTPLRMLMKKIMAVVPSPERFPMFLYKCCSGDPFKMVGAPFTGSS	300
Db	241	LLLLVIVFIPAAWMSLKTPLRMLMKKIMAVVPSPERFPMFLYKCCSGDPFKMVGAPFTGSS	300
Qy	301	LELGWMSPEVPSTLELYVSCHPPRSFAKRIQTLTELQPAELVESDGYPKPSFMPYTAQNSGC	360
Db	301	LELGWMSPEVPSTLELYVSCHPPRSFAKRIQTLTELQPAELVESDGYPKPSFMPYTAQNSGC	360
Qy	361	SAYSEERDRPYGLVSIDVTYVLDAEGPCPTMPCSCBEDDGYPALDLDAGLEBSPGLEDPILD	420
Db	361	SAYSEERDRPYGLVSIDVTYVLDAEGPCPTMPCSCBEDDGYPALDLDAGLEBSPGLEDPILD	420
Qy	421	AGTYTLSCGCCVAGSPGLGGLPGSLDLRLKPLPLADEMDAGGIPMGGRSPGCVSSEAGS	480
Db	421	AGTYTLSCGCCVAGSPGLGGLPGSLDLRLKPLPLADEMDAGGIPMGGRSPGCVSSEAGS	480
Qy	481	PLAGLDMOTFDSGPFVSGDCSSPEVCDFTSPGDEGPRSYLRQVWVYPPPLSPSPQAS	538
Db	481	PLAGLDMOTFDSGPFVSGDCSSPEVCDFTSPGDEGPRSYLRQVWVYPPPLSPSPQAS	538

RESULT 4
US-09-923-246-115
; Sequence 115, Application US/099233246
; Patent No. 660572
; GENERAL INFORMATION:

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? APPLICANT: NO. 6605212AK, JULIA B.
? APPLICANT: Presnell, Scott R.
? APPLICANT: Sprecher, Cindy A.
? APPLICANT: Foster, Donald C.
? APPLICANT: Holly, Richard D.
? APPLICANT: Gross, Jane A.
? APPLICANT: Johnston, Janet V.
? APPLICANT: Nelson, Andrew J.
? APPLICANT: Dillon, Stacey R.
? APPLICANT: Hammond, Angela K.
? TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
? FILE REFERENCE: 99-16
? CURRENT APPLICATION NUMBER: US/09/923,246.
? PRIOR FILING DATE: 2001-08-03
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
? PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
? NUMBER OF SEQ ID NOS: 115
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 115
? LENGTH: 538
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-923-246-115

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Query Match	100.0%;	Score 2958;	DB 2;	Length 538;
Best Local Similarity	100.0%;	Pred. No. 3.6e-267;		
Matches 538;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	I M R G A A P L I L L L L D G M C P D V C T Y D V L Q V I C I L E M W N I A H S U L T I T M O O Y E I K D	60
OY	1 M R G A A P L I L L L L D G M C P D V C T Y D V L Q V I C I L E M W N I A H S U L T I T M O O Y E I K D	60
Dd	1 M R G A A P L I L L L L D G M C P D V C T Y D V L Q V I C I L E M W N I A H S U L T I T M O O Y E I K D	60
OY	61 E A T S C S L H R S A N N A T H A T Y T T C H M D V H F A M A D D I F S V N I T D O S G N Y O E C G S F L A A S I K P	120
Dd	61 E A T S C S L H S A N N A T H A T Y T T C H M D V H F A M A D D I F S V N I T D O S G N Y O E C G S F L A A S I K P	120

QY	121	APPFVATYTSQCYNI	IKMRSDYEDAF	PWLNKCKLQY	ELQYELQYRNRGDPMA	SPRKLLSVDS	180
Db	121	APPFVATYTSQCYNI	IKMRSDYEDAF	PWLNKCKLQY	ELQYELQYRNRGDPMA	SPRKLLSVDS	180
QY	181	RSVSLIPLPEFRKDS	SYELQVRAGP	MPGSSYOGTSE	WSDPVI	FQTOSEELKEGMPHLL	240
Db	181	RSVSLIPLPEFRKDS	SYELQVRAGP	MPGSSYOGTSE	WSDPVI	FQTOSEELKEGMPHLL	240
QY	241	LLILYIVITIPAWSL	KTHPLMRMLK	IKKIAVPS	PERFPMPL	YNGCGSDPKKXMGAPRTGS	300
Db	241	LLILYIVITIPAWSL	KTHPLMRMLK	IKKIAVPS	PERFPMPL	YNGCGSDPKKXMGAPRTGS	300
QY	301	LEIGMSEVEPSTLE	VYSCHPPRSPAK	RLQTELQEPAL	VEVSDGYPKES	FMPAQNSG	360
Db	301	LEIGMSEVEPSTLE	VYSCHPPRSPAK	RLQTELQEPAL	VEVSDGYPKES	FMPAQNSG	360
QY	361	SAYSEBRDRPYGLV	SIDVTYVLDABGP	CTMPCSCEDDGY	PALDLDAGLE	PPSPGLEDPILD	420
Db	361	SAYSEBRDRPYGLV	SIDVTYVLDABGP	CTMPCSCEDDGY	PALDLDAGLE	PPSPGLEDPILD	420
QY	421	AGTYTILSCGCYS	SAGSPGLG	PLGSLDLRLK	PLADGEMD	AGGLPMWGRBRPGVSESEAGS	480
Db	421	AGTYTILSCGCYS	SAGSPGLG	PLGSLDLRLK	PLADGEMD	AGGLPMWGRBRPGVSESEAGS	480
QY	481	PLAGLDMOTFDSG	FPFGSDCSSPVED	CFDTPSGDEG	PPRSYLRQVVI	PPPLASSGPQAS	538
Db	481	PLAGLDMOTFDSG	FPFGSDCSSPVED	CFDTPSGDEG	PPRSYLRQVVI	PPPLASSGPQAS	538

RESULT 5
US-10-295-723-115
; Sequence 115, Application US/10295723
; Patent No. 6686178

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/ GENERATED INFORMATION:
/ APPLICANT: No. 6686178ak, Julia E.
/ APPLICANT: Presnell, Scott R.
/ APPLICANT: Sprecher, Cindy A.
/ APPLICANT: Foster, Donald C.
/ APPLICANT: Holly, Richard D.
/ APPLICANT: Gross, Jane A.
/ APPLICANT: Johnston, Janet V.
/ APPLICANT: Nelson, Andrew J.
/ APPLICANT: Dillon, Tracey R.
/ APPLICANT: Hammond, Angela K.
/ TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAIL LIGAND
/ FILE REFERENCE: 99-16
/ CURRENT APPLICATION NUMBER: US/10/295, 723
/ CURRENT FILING DATE: 2002-11-15
/ PRIOR APPLICATION NUMBER: 09/522,217
/ PRIOR FILING DATE: 2000-03-09
/ PRIOR APPLICATION NUMBER: US 60/123,547
/ PRIOR FILING DATE: 1999-03-09
/ PRIOR APPLICATION NUMBER: US 60/123,904
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 60/142,013
/ PRIOR FILING DATE: 1999-07-01
/ NUMBER OF SEQ ID NOS: 115
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 115
/ LENGTH: 538
/ TYPE: prt
/ ORGANISM: Homo sapiens
US-10-295-723-115

```

Query Match	100.0%;	Score 2958;	DB 2;	Length 538;
Best Local Similarity	100.0%;	Pred. No. 3.6e-267;		
Matches 538;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MPRGMAAPLLLELLLLGGGWCSPDVCYDYLTQTICILEMNNLHSTLTLTWQDQYEELKD 600

DB 1 MPRGMAAPLLLELLLLGGGWCSPDVCYDYLTQTICILEMNNLHSTLTLTWQDQYEELKD 600

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QY 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQECGSLLAESIKP 120
| | | | |
DB 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQECGSLLAESIKP 120
QY 121 APPENVTVTFSGOYNISWRSDYEDPAFYMLKGKLOVELQYRNRGDPMAVSPRRKLISVDS 180
| | | | |
DB 121 APPENVTVTFSGOYNISWRSDYEDPAFYMLKGKLOVELQYRNRGDPMAVSPRRKLISVDS 180
QY 181 RSVALPLERFKDSSYELQVRAGMPGSSYQGTWSEMSDPIVIFQOSEELKEGNPHLL 240
| | | | |
DB 181 RSVALPLERFKDSSYELQVRAGMPGSSYQGTWSEMSDPIVIFQOSEELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTTHPLRLMKKIWA VSPERFMPILYKCGSGDFKKVGA PFRTSS 300
| | | | |
DB 241 LLLLVIFIPAFMSLKTTHPLRLMKKIWA VSPERFMPILYKCGSGDFKKVGA PFRTSS 300
QY 301 LELGPMSEVPSTLEVYSCHPPRSAPAKRLQUTLEQPAELVESDGVKPSFMPAQNOSCG 360
| | | | |
DB 301 LELGPMSEVPSTLEVYSCHPPRSAPAKRLQUTLEQPAELVESDGVKPSFMPAQNOSCG 360
QY 361 SAYSEERDRPYGLVSIOTVTVLDAEGPCCTWPCSCEDDGYPALDLDAGLEBSPGLEDEPLD 420
| | | | |
DB 361 SAYSEERDRPYGLVSIOTVTVLDAEGPCCTWPCSCEDDGYPALDLDAGLEBSPGLEDEPLD 420
QY 421 AGTTVLSGCGVSAGSPGLGPGLSLDRLKPLADGEDMAGLPMGGRSPGVSESEAGS 480
| | | | |
DB 421 AGTTVLSGCGVSAGSPGLGPGLSLDRLKPLADGEDMAGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPQAS 538
| | | | |
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPQAS 538
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RESULT 6
US-10-414-186-2
; Sequence 2, Application US/10414186
; Patent No. 6692924
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6692924ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-186-2
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Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3, 6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MPRGMAAPLULLLLLOGMGCPDLVCYTDYQTYICILEMNNLHPSSTLTLMQOYEEIKD 60
| | | | |
DB 1 MPRGMAAPLULLLLLOGMGCPDLVCYTDYQTYICILEMNNLHPSSTLTLMQOYEEIKD 60
QY 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQECGSLLAESIKP 120
| | | | |
DB 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQECGSLLAESIKP 120
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QY 121 APPENVTVTFSGOYNISWRSDYEDPAFYMLKGKLOVELQYRNRGDPMAVSPRRKLISVDS 180
| | | | |
DB 121 APPENVTVTFSGOYNISWRSDYEDPAFYMLKGKLOVELQYRNRGDPMAVSPRRKLISVDS 180
QY 181 RSVALPLERFKDSSYELQVRAGMPGSSYQGTWSEMSDPIVIFQOSEELKEGNPHLL 240
| | | | |
DB 181 RSVALPLERFKDSSYELQVRAGMPGSSYQGTWSEMSDPIVIFQOSEELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTTHPLRLMKKIWA VSPERFMPILYKCGSGDFKKVGA PFRTSS 300
| | | | |
DB 241 LLLLVIFIPAFMSLKTTHPLRLMKKIWA VSPERFMPILYKCGSGDFKKVGA PFRTSS 300
QY 301 LELGPMSEVPSTLEVYSCHPPRSAPAKRLQUTLEQPAELVESDGVKPSFMPAQNOSCG 360
| | | | |
DB 301 LELGPMSEVPSTLEVYSCHPPRSAPAKRLQUTLEQPAELVESDGVKPSFMPAQNOSCG 360
QY 361 SAYSEERDRPYGLVSIOTVTVLDAEGPCCTWPCSCEDDGYPALDLDAGLEBSPGLEDEPLD 420
| | | | |
DB 361 SAYSEERDRPYGLVSIOTVTVLDAEGPCCTWPCSCEDDGYPALDLDAGLEBSPGLEDEPLD 420
QY 421 AGTTVLSGCGVSAGSPGLGPGLSLDRLKPLADGEDMAGLPMGGRSPGVSESEAGS 480
| | | | |
DB 421 AGTTVLSGCGVSAGSPGLGPGLSLDRLKPLADGEDMAGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPQAS 538
| | | | |
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPQAS 538
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RESULT 7
US-09-825-561A-2
; Sequence 2, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZAPLHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-2
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Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3, 6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MPRGMAAPLULLLLLOGMGCPDLVCYTDYQTYICILEMNNLHPSSTLTLMQOYEEIKD 60
| | | | |
DB 1 MPRGMAAPLULLLLLOGMGCPDLVCYTDYQTYICILEMNNLHPSSTLTLMQOYEEIKD 60
QY 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQECGSLLAESIKP 120
| | | | |
DB 61 EATSCSLHRSANAHATATYTCMDVPHFMADDIFSUNITDQSGNYSQECGSLLAESIKP 120
QY 121 APPENVTVTFSGOYNISWRSDYEDPAFYMLKGKLOVELQYRNRGDPMAVSPRRKLISVDS 180
| | | | |
DB 121 APPENVTVTFSGOYNISWRSDYEDPAFYMLKGKLOVELQYRNRGDPMAVSPRRKLISVDS 180
```

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QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQOSEBELKEGNNPHLL 240
DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQOSEBELKEGNNPHLL 240
QY 241 LLLVIVIPAFWMLKTHPLRLMKKIWAIVSPERFPMPLKYGSGDFKKVVGAPFTGSS 300
DB 241 LLLVIVIPAFWMLKTHPLRLMKKIWAIVSPERFPMPLKYGSGDFKKVVGAPFTGSS 300
QY 301 LELGPMSPBEVSTLEVYSCHPPRSAPKRLQLTLEQEPALVESDGVPRSPFMTAQNNGG 360
DB 301 LELGPMSPBEVSTLEVYSCHPPRSAPKRLQLTLEQEPALVESDGVPRSPFMTAQNNGG 360
QY 361 SAYSEERDRPYGLVSIPTVTVLDAEGPCTWPCSCEDDGPALDLDAGLEPSPGLEDPLD 420
DB 361 SAYSEERDRPYGLVSIPTVTVLDAEGPCTWPCSCEDDGPALDLDAGLEPSPGLEDPLD 420
QY 421 AGTTVLSGCVSAGSPGLGCPGLSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGCPGLSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFVSGDCCSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFVSGDCCSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
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RESULT 8
US-10-243-072-2
; Sequence 2, Application US/10243072
; Patent No. 6803451
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6803451a, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-5551
; CURRENT APPLICATION NUMBER: US/10/243.072
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-072-2
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Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3.6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MPRGMAAPLILLLOGGWGCEDLVCTDYLTQTVICILEMNNLHPSTLTTLTWMODQYEBLKD 60
DB 1 MPRGMAAPLILLLOGGWGCEDLVCTDYLTQTVICILEMNNLHPSTLTTLTWMODQYEBLKD 60
QY 61 EATCSLHRSANNAHTATYTCMDVFFHMADITFSVNTTDSGNVSOCGSGFLAESIKP 120
DB 61 EATCSLHRSANNAHTATYTCMDVFFHMADITFSVNTTDSGNVSOCGSGFLAESIKP 120
QY 121 APPFNVTYTFSGQYNISWRSDEYEDPAFYMLKGKLOYLEQYRNKGDPMVA SPRKLISYDS 180
DB 121 APPFNVTYTFSGQYNISWRSDEYEDPAFYMLKGKLOYLEQYRNKGDPMVA SPRKLISYDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQOSEBELKEGNNPHLL 240
DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQOSEBELKEGNNPHLL 240
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DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQOSEBELKEGNNPHLL 240
QY 241 LLLVIVIPAFWMLKTHPLRLMKKIWAIVSPERFPMPLKYGSGDFKKVVGAPFTGSS 300
DB 241 LLLVIVIPAFWMLKTHPLRLMKKIWAIVSPERFPMPLKYGSGDFKKVVGAPFTGSS 300
QY 301 LELGPMSPBEVSTLEVYSCHPPRSAPKRLQLTLEQEPALVESDGVPRSPFMTAQNNGG 360
DB 301 LELGPMSPBEVSTLEVYSCHPPRSAPKRLQLTLEQEPALVESDGVPRSPFMTAQNNGG 360
QY 361 SAYSEERDRPYGLVSIPTVTVLDAEGPCTWPCSCEDDGPALDLDAGLEPSPGLEDPLD 420
DB 361 SAYSEERDRPYGLVSIPTVTVLDAEGPCTWPCSCEDDGPALDLDAGLEPSPGLEDPLD 420
QY 421 AGTTVLSGCVSAGSPGLGCPGLSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGCPGLSLDLRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFVSGDCCSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFVSGDCCSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
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RESULT 9
US-10-282-622-16
; Sequence 16, Application US/10282622
; Patent No. 6929932
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. 6929932a, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282.622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-622-16
```

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Query Match 100.0%; Score 2958; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 3.6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MPRGMAAPLILLLOGGWGCEDLVCTDYLTQTVICILEMNNLHPSTLTTLTWMODQYEBLKD 60
DB 1 MPRGMAAPLILLLOGGWGCEDLVCTDYLTQTVICILEMNNLHPSTLTTLTWMODQYEBLKD 60
QY 61 EATCSLHRSANNAHTATYTCMDVFFHMADITFSVNTTDSGNVSOCGSGFLAESIKP 120
DB 61 EATCSLHRSANNAHTATYTCMDVFFHMADITFSVNTTDSGNVSOCGSGFLAESIKP 120
QY 121 APPFNVTYTFSGQYNISWRSDEYEDPAFYMLKGKLOYLEQYRNKGDPMVA SPRKLISYDS 180
DB 121 APPFNVTYTFSGQYNISWRSDEYEDPAFYMLKGKLOYLEQYRNKGDPMVA SPRKLISYDS 180
QY 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQOSEBELKEGNNPHLL 240
DB 181 RSVSLLPLEFRKDSYELQVRAGMPGSSYOGTWSWSDPVIPTQOSEBELKEGNNPHLL 240
QY 241 LLLVIVIPAFWMLKTHPLRLMKKIWAIVSPERFPMPLKYGSGDFKKVVGAPFTGSS 300
DB 241 LLLVIVIPAFWMLKTHPLRLMKKIWAIVSPERFPMPLKYGSGDFKKVVGAPFTGSS 300
QY 301 LELGPMSPBEVSTLEVYSCHPPRSAPKRLQLTLEQEPALVESDGVPRSPFMTAQNNGG 360
DB 301 LELGPMSPBEVSTLEVYSCHPPRSAPKRLQLTLEQEPALVESDGVPRSPFMTAQNNGG 360
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Qy 361 SAYSEEDRPYGLVSIIDTVTLDAEGPCTMPCSCEDDGYPALDLDAGLSPSGLEDPLLD 420
Db 361 SAYSEEDRPYGLVSIIDTVTLDAEGPCTMPCSCEDDGYPALDLDAGLSPSGLEDPLLD 420
Qy 421 AGTVLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Db 421 AGTVLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Qy 481 PLAGLMDTDFSGVSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
Db 481 PLAGLMDTDFSGVSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538

RESULT 10
US-09-949-016-11544
; Sequence 11544, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11544
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11544

Query Match 100.0%; Score 2958; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 3.6e-267;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAPLILLLLQGGMGCPDLVCYTDYLOTVICILEMNLHPSSTLTLTWODQYELKD 60
Db 1 MPRGMAPLILLLLQGGMGCPDLVCYTDYLOTVICILEMNLHPSSTLTLTWODQYELKD 69
Qy 61 EATSCSLHRSANATHATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLLAESIKP 120
Db 70 EATSCSLHRSANATHATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLLAESIKP 129
Qy 121 APPENVTVTSGQYNIWRSRSDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRKLISYDS 180
Db 130 APPENVTVTSGQYNIWRSRSDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRKLISYDS 189
Qy 181 RSVSLPLEFRKDSYELQVAPGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNPHLL 240
Db 190 RSVSLPLEFRKDSYELQVAPGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNPHLL 249
Qy 241 LLLLVIVFIPAFWMLKTHPLRLMKKIWAIVSPERFEMPLYKCGSGDFKKNVGAFTGSS 300
Db 250 LLLLVIVFIPAFWMLKTHPLRLMKKIWAIVSPERFEMPLYKCGSGDFKKNVGAFTGSS 309
Qy 301 LEIGPMSPEVPSSTLEVSYCHPSPAPAKRLQITELQEPALVESDGVKPSFWPTAQNSGG 360
Db 310 LEIGPMSPEVPSSTLEVSYCHPSPAPAKRLQITELQEPALVESDGVKPSFWPTAQNSGG 369
Qy 361 SAYSEEDRPYGLVSIIDTVTLDAEGPCTMPCSCEDDGYPALDLDAGLSPSGLEDPLLD 420
Db 370 SAYSEEDRPYGLVSIIDTVTLDAEGPCTMPCSCEDDGYPALDLDAGLSPSGLEDPLLD 429
Qy 421 AGTVLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
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Db 430 AGTVLSCGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 489
Qy 481 PLAGLMDTDFSGVSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 538
Db 490 PLAGLMDTDFSGVSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPOAS 547

RESULT 11
US-09-825-561A-65
; Sequence 65, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holley, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 568
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-825-561A-65

Query Match 95.2%; Score 2817; DB 2; Length 568;
Best Local Similarity 89.9%; Pred. No. 5.6e-254;
Matches 523; Conservative 0; Mismatches 1; Indels 58; Gaps 3;

Qy 1 MPRGMAPLILLLLQGGMGCPDLVCYTDYLOTVI 34
Db 1 MPRGMAPLILLLLQGGMGCPDLVCYTDYLOTVI 60
Qy 35 CILEMNLHPSSTLTLTW-----QDYELKDEATSCSLHRSANATH 76
Db 61 CILEMNLHPSSTLTLTWIISNNTGCIYKDRITLDRQYELKDEATSCSLHRSANATH 120
Qy 77 ATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLLAESIKPAPPENVTVTSGQYNI 136
Db 121 ATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLLAESIKPAPPENVTVTSGQYNI 166
Qy 137 SMSRDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRKLISYDSRSVSLPLEFRKDSY 196
Db 167 SMSRDYEDPAFYMLKGLQYELQYRNRGDPMAVSPRRKLISYDSRSVSLPLEFRKDSY 226
Qy 197 ELQVAPGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNPHLLLLLVIVFIPAFWSLK 256
Db 227 ELQVAPGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNPHLLLLLVIVFIPAFWSLK 286
Qy 287 THPLRLMKKIWAIVSPERFEMPLYKCGSGDFKKNVGAFTGSSSLEIGPMSPEVPSSTLEV 346
Db 257 THPLRLMKKIWAIVSPERFEMPLYKCGSGDFKKNVGAFTGSSSLEIGPMSPEVPSSTLEV 316
Qy 317 YSCHPSPAPAKRLQITELQEPALVESDGVKPSFWPTAQNSGSAyseEDRPYGLVSI 376
Db 347 YSCHPSPAPAKRLQITELQEPALVESDGVKPSFWPTAQNSGSAyseEDRPYGLVSI 406
Qy 407 DTVTLDAEGPCTMPCSCEDDGYPALDLDAGLSPSGLEDPLLDAGTVLSCGCVSAGSP 436
Db 437 DTVTLDAEGPCTMPCSCEDDGYPALDLDAGLSPSGLEDPLLDAGTVLSCGCVSAGSP 466
Qy 467 GLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGSPLAGLMDTDFSGV 526
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Qy 497 SDGSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPOAS 538
Db 527 SDGSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPOAS 568

RESULT 12

US-09-404-641-85
; Sequence 85, Application US/09404641
; Patent No. 6576744
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6576744ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAP1HA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-404-641-85

Query Match 58.7%; Score 1735.5; DB 2; Length 529;
Best Local Similarity 62.7%; Pred. No. 4,66-153;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

Qy 1 MPRGMAAPLILLILLOQMGCPDLVCYTDYLOTVCILEMNLHPSTLTLMQDOYEELKD 60
Db 1 MPRGPVALILLILHGAWSCDLCTCYTDYLTITCVELTRSPNPSILSTLMQDEYEELQD 60
Qy 61 EATCSLHRSAHNTHATYTCMDVHFHMADDFSVNITDOSGNSOCSGFFLAESIKP 120
Db 61 QETCSLHRSAHNTHATYTCMDVHFHMADDFSVNITDOSGNSOCSGFFLAESIKP 120
Qy 121 APPENVVTFSGOYNISWRSDYEDPAFMYLKGKLOYLEQYRNRPDMVAVSPRRKLISVDS 180
Db 121 APPENVVTFSGOYNISWRSDYEDPAFMYLKGKLOYLEQYRNRPDMVAVSPRRKLISVDS 180
Qy 181 RSVSLPLLEFRKDSYELQVRAQPMPPGSSYOGTWSWSDPYIFOTQSEELKEGNNPHLL 240
Db 181 RSVSLPLLEFRKDSYELQVRAQPMPPGSSYOGTWSWSDPYIFOTQSEELKEGNNPHLL 240
Qy 241 LLLVYVTFPFWSLKTHPLRLMKKIYA-VPSBRFPMPLYKGCSSGPFKKVGAAPFTGS 299
Db 241 LLLVYVTFPFWSLKTHPLRLMKKIYA-VPSBRFPMPLYKGCSSGPFKKVGAAPFTGS 299
Qy 241 LLLVYVTFPFWSLKTHPLRLMKKIYA-VPSBRFPMPLYKGCSSGPFKKVGAAPFTGS 299
Db 241 LLLVYVTFPFWSLKTHPLRLMKKIYA-VPSBRFPMPLYKGCSSGPFKKVGAAPFTGS 299
Qy 300 SLELGPMSPEVSTLEVYSCHPRPSPAKRLQUTLEQBPALVESDGVKPSFW--PTAQ 356
Db 300 SLELGPMSPEVSTLEVYSCHPRPSPAKRLQUTLEQBPALVESDGVKPSFW--PTAQ 356
Qy 357 NSGSAVSEERDRPYGLVSDITVTLDAEGPCTWPCSCEDDGYPALDADAGLESPGLE 416
Db 357 NSGSAVSEERDRPYGLVSDITVTLDAEGPCTWPCSCEDDGYPALDADAGLESPGLE 416
Qy 417 PLDAGTIVLSCGCVSAGSPGLGSLDLRLKPLADGEMAGGLPMWGRSGCGVSES 476
Db 417 PLDAGTIVLSCGCVSAGSPGLGSLDLRLKPLADGEMAGGLPMWGRSGCGVSES 476
Qy 477 EAGSPPLAGLMDTDFSGFVSGSDSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPO 536
Db 477 EAGSPPLAGLMDTDFSGFVSGSDSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPO 536
Qy 475 EAGSP-PLDMDTDFSGFVSGSDSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPO 527
Db 475 EAGSP-PLDMDTDFSGFVSGSDSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPO 527

Qy 537 AS 538
Db 528 SS 529

RESULT 13

US-10-414-186-85
; Sequence 85, Application US/10414186
; Patent No. 6692924
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. 6692924ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAP1HA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-414-186-85

Query Match 58.7%; Score 1735.5; DB 2; Length 529;
Best Local Similarity 62.7%; Pred. No. 4,66-153;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

Qy 1 MPRGMAAPLILLILLOQMGCPDLVCYTDYLOTVCILEMNLHPSTLTLMQDOYEELKD 60
Db 1 MPRGPVALILLILHGAWSCDLCTCYTDYLTITCVELTRSPNPSILSTLMQDEYEELQD 60
Qy 61 EATCSLHRSAHNTHATYTCMDVHFHMADDFSVNITDOSGNSOCSGFFLAESIKP 120
Db 61 QETCSLHRSAHNTHATYTCMDVHFHMADDFSVNITDOSGNSOCSGFFLAESIKP 120
Qy 121 APPENVVTFSGOYNISWRSDYEDPAFMYLKGKLOYLEQYRNRPDMVAVSPRRKLISVDS 180
Db 121 APPENVVTFSGOYNISWRSDYEDPAFMYLKGKLOYLEQYRNRPDMVAVSPRRKLISVDS 180
Qy 181 RSVSLPLLEFRKDSYELQVRAQPMPPGSSYOGTWSWSDPYIFOTQSEELKEGNNPHLL 240
Db 181 RSVSLPLLEFRKDSYELQVRAQPMPPGSSYOGTWSWSDPYIFOTQSEELKEGNNPHLL 240
Qy 241 LLLVYVTFPFWSLKTHPLRLMKKIYA-VPSBRFPMPLYKGCSSGPFKKVGAAPFTGS 299
Db 241 LLLVYVTFPFWSLKTHPLRLMKKIYA-VPSBRFPMPLYKGCSSGPFKKVGAAPFTGS 299
Qy 241 LLLVYVTFPFWSLKTHPLRLMKKIYA-VPSBRFPMPLYKGCSSGPFKKVGAAPFTGS 299
Db 241 LLLVYVTFPFWSLKTHPLRLMKKIYA-VPSBRFPMPLYKGCSSGPFKKVGAAPFTGS 299
Qy 300 SLELGPMSPEVSTLEVYSCHPRPSPAKRLQUTLEQBPALVESDGVKPSFW--PTAQ 356
Db 300 SLELGPMSPEVSTLEVYSCHPRPSPAKRLQUTLEQBPALVESDGVKPSFW--PTAQ 356
Qy 357 NSGSAVSEERDRPYGLVSDITVTLDAEGPCTWPCSCEDDGYPALDADAGLESPGLE 416
Db 357 NSGSAVSEERDRPYGLVSDITVTLDAEGPCTWPCSCEDDGYPALDADAGLESPGLE 416
Qy 417 PLDAGTIVLSCGCVSAGSPGLGSLDLRLKPLADGEMAGGLPMWGRSGCGVSES 476
Db 417 PLDAGTIVLSCGCVSAGSPGLGSLDLRLKPLADGEMAGGLPMWGRSGCGVSES 476
Qy 477 EAGSPPLAGLMDTDFSGFVSGSDSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPO 536
Db 477 EAGSPPLAGLMDTDFSGFVSGSDSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPO 536
Qy 475 EAGSP-PLDMDTDFSGFVSGSDSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPO 527
Db 475 EAGSP-PLDMDTDFSGFVSGSDSPVECDTTSRDEGPPRSYLRQWVIRPPPLSSPGPO 527

OY 537 AS 538
Db 528 SS 529

RESULT 14
US-09-825-561A-12
Sequence 12, Application US/09825561A
Patent No. 677539
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 677539ak, Julia E.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZAPLHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 529
TYPE: PRT
ORGANISM: mus musculus
US-09-825-561A-12

Query Match 58.7%; Score 1735.5; DB 2; Length 529;
Best Local Similarity 62.7%; Pred. No. 4,66-153;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

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Db 1 MPRGPVALLLILLHGMASCLDLTCYDYIMTITCVLETRSPNPSILSTLMODEYELQD 60
OY 61 EATSCSLHRSANATHTATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLAESIKP 120
Db 61 QETFCSLHRSCHNTHTIWTCHMRLSQFLSDEVFVAVNTDQSGNNSQEGCSFVLAESIKP 120
OY 121 APPFNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLIISVDS 180
Db 121 APPFNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLIISVDS 180
OY 181 RSVSLPLEFRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFOTQSEBELKEGNPHLL 240
Db 181 RNVSLPLEFRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFOTQSEBELKEGNPHLL 240
OY 241 LLLLVIFIPAFWSLKTHTPLRLWKTIWA-VPSPERFEMPLKXGCGDFKXKMGVAPRTGS 299
Db 241 LLLLVIFIPAFWSLKTHTPLRLWKTIWA-VPSPERFEMPLKXGCGDFKXKMGVAPRTGS 299
OY 300 SLEIGPMSPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFW---PTAQ 356
Db 300 SLEIGPMSPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFW---PTAQ 356
OY 357 NSGSAVSEERDRYGLVSDITVTVDABEPCCTWPCSCEDDGYPALDLDALEBSPGLEED 416
Db 357 NSGSAVSEERDRYGLVSDITVTVDABEPCCTWPCSCEDDGYPALDLDALEBSPGLEED 416
OY 417 PLIDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
Db 417 PLIDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
OY 477 EAGSPPLAGLMDFTDGSFVSGDCSSPVECDFTSPGDEGPRPSYLRQWVVIIPPLSSPGPQ 536
Db 477 EAGSPPLAGLMDFTDGSFVSGDCSSPVECDFTSPGDEGPRPSYLRQWVVIIPPLSSPGPQ 536

OY 537 AS 538
Db 528 SS 529

RESULT 15
US-10-243-072-85
Sequence 85, Application US/10243072
Patent No. 6803451
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Conklin, Darrell C.
APPLICANT: No. 6803451ak, Julia E.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
FILE REFERENCE: 98-55C1
CURRENT APPLICATION NUMBER: US/10/243,072
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/628,127
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/100,896
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: US 60/123,546
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: US 09/404,641
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 529
TYPE: PRT
ORGANISM: Mus musculus
US-10-243-072-85

Query Match 58.7%; Score 1735.5; DB 2; Length 529;
Best Local Similarity 62.7%; Pred. No. 4,66-153;
Matches 340; Conservative 49; Mismatches 136; Indels 17; Gaps 6;

OY 1 MPRGMAPLLILLLOGGMCPDLVCTYDYIQTIVICILEMNNLHPSTLTLMODQYBELKD 60
Db 1 MPRGPVALLLILLHGMASCLDLTCYDYIMTITCVLETRSPNPSILSTLMODEYELQD 60
OY 61 EATSCSLHRSANATHTATYTCMDVHFHMADDFSVNITDQSGNYSQEGCSFLAESIKP 120
Db 61 QETFCSLHRSCHNTHTIWTCHMRLSQFLSDEVFVAVNTDQSGNNSQEGCSFVLAESIKP 120
OY 121 APPFNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLIISVDS 180
Db 121 APPFNVTFTSGQYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLIISVDS 180
OY 181 RSVSLPLEFRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFOTQSEBELKEGNPHLL 240
Db 181 RNVSLPLEFRKDSYELQVRAGMPGSSYQGTWSEMSDPVIFOTQSEBELKEGNPHLL 240
OY 241 LLLLVIFIPAFWSLKTHTPLRLWKTIWA-VPSPERFEMPLKXGCGDFKXKMGVAPRTGS 299
Db 241 LLLLVIFIPAFWSLKTHTPLRLWKTIWA-VPSPERFEMPLKXGCGDFKXKMGVAPRTGS 299
OY 300 SLEIGPMSPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFW---PTAQ 356
Db 300 SLEIGPMSPEVSTLEVYSCHPPRSPAKRLQTLQEPALVESDGVKPSFW---PTAQ 356
OY 357 NSGSAVSEERDRYGLVSDITVTVDABEPCCTWPCSCEDDGYPALDLDALEBSPGLEED 416
Db 357 NSGSAVSEERDRYGLVSDITVTVDABEPCCTWPCSCEDDGYPALDLDALEBSPGLEED 416
OY 417 PLIDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
Db 417 PLIDAGTTVSLCCGVASGPGGLGSLDLRLKPLADGEDMAGGLPMWGRSPGVSES 476
OY 477 EAGSPPLAGLMDFTDGSFVSGDCSSPVECDFTSPGDEGPRPSYLRQWVVIIPPLSSPGPQ 536
Db 477 EAGSPPLAGLMDFTDGSFVSGDCSSPVECDFTSPGDEGPRPSYLRQWVVIIPPLSSPGPQ 536

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Qy	537	AS 538	
	:		
Db	528	SS 529	

Search completed: September 7, 2006, 12:53:37
Job time : 55.8 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:52:41; Search time 195.217 Seconds
(without alignment)
1276.576 Million cell updates/sec

Title: US-10-659-684-115

Perfect score: 2958
Sequence: 1 MPRGMAAPLLLLLOQSGMGC.....YLRQWVYIPPLSPGQAS 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications MA Main:*

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- 2: /EMC_CeJerra_SIDS3/ptodata/2/pubppa/US08_PUBCOMB.pep:*
- 3: /EMC_CeJerra_SIDS3/ptodata/2/pubppa/US09_PUBCOMB.pep:*
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- 6: /EMC_CeJerra_SIDS3/ptodata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2958	100.0	538	3	US-09-965-313-2 Sequence 2, Appli
2	2958	100.0	538	3	US-09-923-246-115 Sequence 115, App
3	2958	100.0	538	3	US-09-825-561A-2 Sequence 2, Appli
4	2958	100.0	538	3	US-09-972-218A-2 Sequence 2, Appli
5	2958	100.0	538	4	US-10-264-634-2 Sequence 2, Appli
6	2958	100.0	538	4	US-10-295-723-115 Sequence 115, App
7	2958	100.0	538	4	US-10-282-622-16 Sequence 16, Appli
8	2958	100.0	538	4	US-10-243-072-2 Sequence 2, Appli
9	2958	100.0	538	4	US-10-414-186-2 Sequence 2, Appli
10	2958	100.0	538	4	US-10-456-780-6 Sequence 6, Appli
11	2958	100.0	538	4	US-10-655-684-115 Sequence 115, App
12	2958	100.0	538	4	US-10-620-169-4 Sequence 4, Appli
13	2958	100.0	538	4	US-10-715-998-2 Sequence 2, Appli
14	2958	100.0	538	5	US-10-872-087-2 Sequence 2, Appli
15	2958	100.0	538	5	US-10-787-442-115 Sequence 115, App
16	2958	100.0	538	5	US-10-798-380-43 Sequence 43, Appli
17	2958	100.0	538	5	US-10-864-249-2 Sequence 2, Appli
18	2958	100.0	538	5	US-10-951-239-10 Sequence 10, Appli
19	2958	100.0	538	6	US-11-174-398-16 Sequence 16, Appli
20	2958	100.0	538	6	US-11-133-947-6 Sequence 6, Appli
21	2958	100.0	538	6	US-11-197-488-2 Sequence 2, Appli
22	2951	99.8	538	3	US-09-758-664-2 Sequence 2, Appli
23	2817	95.2	568	3	US-09-825-561A-65 Sequence 65, Appli
24	2817	95.2	568	5	US-10-872-087-65 Sequence 65, Appli
25	2817	95.2	568	5	US-09-825-561A-12 Sequence 12, Appli
26	1735.5	58.7	529	3	US-09-972-218A-10 Sequence 10, Appli
27	1735.5	58.7	529	3	US-09-972-218A-10 Sequence 10, Appli

28	1735.5	58.7	529	4	US-10-264-634-10 Sequence 10, Appli
29	1735.5	58.7	529	4	US-10-243-072-85 Sequence 85, Appli
30	1735.5	58.7	529	4	US-10-414-186-85 Sequence 85, Appli
31	1735.5	58.7	529	4	US-10-418-450-2 Sequence 2, Appli
32	1735.5	58.7	529	4	US-10-715-998-85 Sequence 85, Appli
33	1735.5	58.7	529	5	US-10-872-087-12 Sequence 12, Appli
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36	1735.5	58.7	529	6	US-11-132-947-8 Sequence 8, Appli
37	1735.5	58.7	529	6	US-11-197-488-10 Sequence 10, Appli
38	1729.5	58.5	529	3	US-09-965-313-4 Sequence 4, Appli
39	1729.5	58.5	529	3	US-09-732-234-6 Sequence 6, Appli
40	1729.5	58.5	529	3	US-09-784-859-6 Sequence 6, Appli
41	1729.5	58.5	529	4	US-10-076-840-6 Sequence 6, Appli
42	1729.5	58.5	529	4	US-10-624-044-6 Sequence 6, Appli
43	1729.5	58.5	529	5	US-10-415-440-6 Sequence 6, Appli
44	1591	53.8	289	3	US-09-941-973-2 Sequence 2, Appli
45	1302	44.0	384	6	US-11-075-351-32 Sequence 32, Appli

ALIGNMENTS

RESULT 1									
US-09-965-313-2									
Sequence 2, Application US/09965313									
Patent No. US20020090680A1									
GENERAL INFORMATION:									
APPLICANT: Hodge, Martin R.									
TITLE OF INVENTION: No. US20020090680A1 IL-9/IL-2 Receptor-like Molecules									
TITLE OF INVENTION: and Uses Thereof									
FILE REFERENCE: 5800-17A									
CURRENT APPLICATION NUMBER: US/09/965,313									
CURRENT FILING DATE: 2001-09-26									
PRIOR APPLICATION NUMBER: US 09/313,913									
PRIOR FILING DATE: 1999-05-18									
NUMBER OF SEQ ID NOS: 8									
SOFTWARE: FastSeq for Windows Version 3.0									
SEQ ID NO 2									
LENGTH: 538									
TYPE: PRT									
ORGANISM: Homo sapiens IL-2/IL-9 Receptor Like									
US-09-965-313-2									
Query Match									
Best Local Similarity 100.0%; Score 2958; DB 3; Length 538;									
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	MPRGMAAPLLLLLOQSGMGC	PDLYCYDTYLTQVLCILEMNLHPS	TLTLTWQDYEBELKD	60				
QY	61	EATCSLHRSANHTATYTCHMDVFHFMADDFSVNITDQSGNVSQEGCSFLLAESIKP	120						
DB	61	EATCSLHRSANHTATYTCHMDVFHFMADDFSVNITDQSGNVSQEGCSFLLAESIKP	120						
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QY	181	RSVGLLPLEPRKDSYELQVAGMPGSSVYQGTSEMSDPVITFOTQSEBELKEGNPHLL	240						
DB	181	RSVGLLPLEPRKDSYELQVAGMPGSSVYQGTSEMSDPVITFOTQSEBELKEGNPHLL	240						
QY	241	LLLVIVFI	PAFWSLKTHTPLRLWKKI	WAVSPERFMP	LYKSGCDFKKNVGA	PFTGSS	300		
DB	241	LLLVIVFI	PAFWSLKTHTPLRLWKKI	WAVSPERFMP	LYKSGCDFKKNVGA	PFTGSS	300		
QY	301	LELPMSPEVSTLEVS	CHPPSPAKRLQITELQEPALVES	GVGKPSFWPTA	QNSGG	360			
DB	301	LELPMSPEVSTLEVS	CHPPSPAKRLQITELQEPALVES	GVGKPSFWPTA	QNSGG	360			
QY	361	SAYSEBRDPRYGLV	SIDVTYTLDAEGPCTWCSCEDDGY	PALDDAGLEPFGLEDPLD	420				

Db 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYALDLADAGLEBPGLJEDLDD 420
Qy 421 AGTTVLSGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Qy 481 PLGLMDPTDPSGVSQSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPQAS 538
Db 481 PLGLMDPTDPSGVSQSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPQAS 538

RESULT 2
US-09-923-246-115

Sequence 115, Application US/09923246
Patent No. US2002012846A1
GENERAL INFORMATION:
APPLICANT: No. US2002012846A1ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Groes, Jane A.
APPLICANT: Johnson, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923, 246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-09-923-246-115

Query Match 100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAPLILLLOGGMGCPDLVCTYDYLQTVICILEMNLHPSTLTITWQDQYEEIKD 60
Db 1 MPRGMAPLILLLOGGMGCPDLVCTYDYLQTVICILEMNLHPSTLTITWQDQYEEIKD 60
Qy 61 EATSCSLHRSANAHATYTCMDVFFHFMADDFSVNITDQSGNYSQEGCSFLLAESIKP 120
Db 61 EATSCSLHRSANAHATYTCMDVFFHFMADDFSVNITDQSGNYSQEGCSFLLAESIKP 120
Qy 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNKGDPMVA5PRKLI5VDS 180
Db 121 APPENVTVTFSGQYNISWRSYEDPAFYMLKGLQYELQYRNKGDPMVA5PRKLI5VDS 180
Qy 181 RSVSLPLERFKDSSYELQVRAGPMGSSYQGTWSESDVITQTOSEELKEGNPHLL 240
Db 181 RSVSLPLERFKDSSYELQVRAGPMGSSYQGTWSESDVITQTOSEELKEGNPHLL 240
Qy 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWA5PSPERFMPLYKGCSDPFKMWGAPFTGSS 300
Db 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWA5PSPERFMPLYKGCSDPFKMWGAPFTGSS 300
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Db 301 LEIGPMSPVSTLEVYSCHPPSPAKRLQTLQEPALVESDGVKPSFWPTAQN5SGG 360

Qy 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYALDLADAGLEBPGLJEDLDD 420
Db 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYALDLADAGLEBPGLJEDLDD 420
Qy 421 AGTTVLSGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Db 421 AGTTVLSGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
Qy 481 PLGLMDPTDPSGVSQSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPQAS 538
Db 481 PLGLMDPTDPSGVSQSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPQAS 538

RESULT 3

US-09-825-561A-2
Sequence 2, Application US/09825561A
Patent No. US2002013767A1
GENERAL INFORMATION:
APPLICANT: No. US2002013767A1ak, Julia E.
APPLICANT: Sprecher, Cindy A.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-09-825-561A-2

Query Match 100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAPLILLLOGGMGCPDLVCTYDYLQTVICILEMNLHPSTLTITWQDQYEEIKD 60
Db 1 MPRGMAPLILLLOGGMGCPDLVCTYDYLQTVICILEMNLHPSTLTITWQDQYEEIKD 60
Qy 61 EATSCSLHRSANAHATYTCMDVFFHFMADDFSVNITDQSGNYSQEGCSFLLAESIKP 120
Db 61 EATSCSLHRSANAHATYTCMDVFFHFMADDFSVNITDQSGNYSQEGCSFLLAESIKP 120
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Qy 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYALDLADAGLEBPGLJEDLDD 420
Db 361 SAYSEERDRPYGLVSIIDTVTVLDAEGPCTWPCSCEDDGYALDLADAGLEBPGLJEDLDD 420
Qy 421 AGTTVLSGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480

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Db      421 |||||
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Db      481 PLAGLMDTDFSGVSGSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPLSSPPQAS 538

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RESULT 4
US-09-972-218A-2
; Sequence 2, Application US/09972218A
; Publication No. US20030049798A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Laura
; APPLICANT: Whitters, Matthew J
; APPLICANT: Collins, Mary
; APPLICANT: Young, Deborah A.
; APPLICANT: Donaldson, Debra D.
; APPLICANT: Lowe, Leslie D.
; APPLICANT: Unger, Michelle
; TITLE OF INVENTION: MU-1, Member of the Cytokine Receptor Family
; FILE REFERENCE: 22058-552CIP2
; CURRENT APPLICATION NUMBER: US/09/972,218A
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/569384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/560766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US/6057228
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
US-09-972-218A-2

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Query Match      100.0%; Score 2958; DB 3; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 EATSCSLHRSANNAHTATYTCMDVFFHMDLFSVNTIQQSGVSGECSFLAESTIKP 120
Qy      121 APPFNVTFTSGOYNISMRSDYEDPAFYMLKGLQYELQYRNKDPMAVSPRRKLISVDS 180
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Qy      181 RSVSLPLERFKDSSYELQYRAGMPGSSYQGTWSEMSDPVIFOTOSBELKEGNNPHLL 240
Db      181 RSVSLPLERFKDSSYELQYRAGMPGSSYQGTWSEMSDPVIFOTOSBELKEGNNPHLL 240
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Qy      301 LEIGPMSPEVPSTLEVYSCHPSPRPAKRLQLTTELQEPALVESDGVKPSFMPPTAONSGG 360
Db      301 LEIGPMSPEVPSTLEVYSCHPSPRPAKRLQLTTELQEPALVESDGVKPSFMPPTAONSGG 360
Qy      361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCEDDGYPALDIDAGLEPSPGLEDPLD 420
Db      361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCEDDGYPALDIDAGLEPSPGLEDPLD 420
Qy      421 AGTTVSLCCGVASASPGIGPGLSLDLRLKPLADGEDMAGGLPMGGSPPGVSESEAGS 480
Db      421 AGTTVSLCCGVASASPGIGPGLSLDLRLKPLADGEDMAGGLPMGGSPPGVSESEAGS 480

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Qy      481 PLAGLMDTDFSGVSGSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPLSSPPQAS 538
Db      481 PLAGLMDTDFSGVSGSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPLSSPPQAS 538

```

```

RESULT 5
US-10-264-634-2
; Sequence 2, Application US/10264634
; Publication No. US20030108549A1
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Debra et al.
; TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor Activity
; FILE REFERENCE: G15320-P3
; CURRENT APPLICATION NUMBER: US/10/264,634
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 09/040,005
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 09/560,766
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/569,384
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 09/972,218
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/373,746
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
US-10-264-634-2

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```

Query Match      100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 MPRGMAAPLLLLLQGGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTWQDQYEEBKD 60
Db      1 MPRGMAAPLLLLLQGGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTWQDQYEEBKD 60
Qy      61 EATSCSLHRSANNAHTATYTCMDVFFHMDLFSVNTIQQSGVSGECSFLAESTIKP 120
Db      61 EATSCSLHRSANNAHTATYTCMDVFFHMDLFSVNTIQQSGVSGECSFLAESTIKP 120
Qy      121 APPFNVTFTSGOYNISMRSDYEDPAFYMLKGLQYELQYRNKDPMAVSPRRKLISVDS 180
Db      121 APPFNVTFTSGOYNISMRSDYEDPAFYMLKGLQYELQYRNKDPMAVSPRRKLISVDS 180
Qy      181 RSVSLPLERFKDSSYELQYRAGMPGSSYQGTWSEMSDPVIFOTOSBELKEGNNPHLL 240
Db      181 RSVSLPLERFKDSSYELQYRAGMPGSSYQGTWSEMSDPVIFOTOSBELKEGNNPHLL 240
Qy      241 LLLLVYFIAPFMSLKTTHPLMRMLKKTIAVSPERFPMPLKKGSGPFKKWVGAPFTGSS 300
Db      241 LLLLVYFIAPFMSLKTTHPLMRMLKKTIAVSPERFPMPLKKGSGPFKKWVGAPFTGSS 300
Qy      301 LEIGPMSPEVPSTLEVYSCHPSPRPAKRLQLTTELQEPALVESDGVKPSFMPPTAONSGG 360
Db      301 LEIGPMSPEVPSTLEVYSCHPSPRPAKRLQLTTELQEPALVESDGVKPSFMPPTAONSGG 360
Qy      361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCEDDGYPALDIDAGLEPSPGLEDPLD 420
Db      361 SAYSEERDRPYGLVSIITVTVLDAEGPCTWPCSCEDDGYPALDIDAGLEPSPGLEDPLD 420
Qy      421 AGTTVSLCCGVASASPGIGPGLSLDLRLKPLADGEDMAGGLPMGGSPPGVSESEAGS 480
Db      421 AGTTVSLCCGVASASPGIGPGLSLDLRLKPLADGEDMAGGLPMGGSPPGVSESEAGS 480
Qy      481 PLAGLMDTDFSGVSGSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPLSSPPQAS 538
Db      481 PLAGLMDTDFSGVSGSDCSSPVCECDFTSPGDEGPPRSYLRQWVVIIPPLSSPPQAS 538

```

RESULT 6
US-10-295-723-115
; Sequence 115, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-115

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLGCGMGPDLVCTDYDTQTVICILEMNNLHPSTLTLTWQDQYELKD 60
DB 1 MPRGMAAPLLLLLLGCGMGPDLVCTDYDTQTVICILEMNNLHPSTLTLTWQDQYELKD 60
QY 61 EATSCSLHRSANAHNATHTYTCMDVHFHMADDFSVNITDQSGVYSGECSFLAESIKP 120
DB 61 EATSCSLHRSANAHNATHTYTCMDVHFHMADDFSVNITDQSGVYSGECSFLAESIKP 120
QY 121 APPNNVTVTSSGQYNISWRSYEDPAFYMLKGKIQLEYLQYRNKDPMAVSPRRKLISVDS 180
DB 121 APPNNVTVTSSGQYNISWRSYEDPAFYMLKGKIQLEYLQYRNKDPMAVSPRRKLISVDS 180
QY 121 APPNNVTVTSSGQYNISWRSYEDPAFYMLKGKIQLEYLQYRNKDPMAVSPRRKLISVDS 180
DB 121 APPNNVTVTSSGQYNISWRSYEDPAFYMLKGKIQLEYLQYRNKDPMAVSPRRKLISVDS 180
QY 181 RSVSLPLERKDSYELQVRAGMPGSSYQGTWSEMSDPIVFTQOSEELKEGNNPHLL 240
DB 181 RSVSLPLERKDSYELQVRAGMPGSSYQGTWSEMSDPIVFTQOSEELKEGNNPHLL 240
QY 181 RSVSLPLERKDSYELQVRAGMPGSSYQGTWSEMSDPIVFTQOSEELKEGNNPHLL 240
DB 181 RSVSLPLERKDSYELQVRAGMPGSSYQGTWSEMSDPIVFTQOSEELKEGNNPHLL 240
QY 241 LLLLVIFIPAFMSLKTTHPLMKKIWAVPSPERFMPLYKGGSGDFKKVGAFTGSS 300
DB 241 LLLLVIFIPAFMSLKTTHPLMKKIWAVPSPERFMPLYKGGSGDFKKVGAFTGSS 300
QY 241 LLLLVIFIPAFMSLKTTHPLMKKIWAVPSPERFMPLYKGGSGDFKKVGAFTGSS 300
DB 241 LLLLVIFIPAFMSLKTTHPLMKKIWAVPSPERFMPLYKGGSGDFKKVGAFTGSS 300
QY 301 LEIGPMSPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVKPPSPFTAQNSSG 360
DB 301 LEIGPMSPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVKPPSPFTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIIDTVVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLJEDPLD 420
DB 361 SAYSEERDRPYGLVSIIDTVVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLJEDPLD 420
QY 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGDMAGGLPMWGRSPGVSESEAGS 480
DB 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGDMAGGLPMWGRSPGVSESEAGS 480

QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPOAS 538
RESULT 7
US-10-282-622-16
; Sequence 16, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-622-16

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLGCGMGPDLVCTDYDTQTVICILEMNNLHPSTLTLTWQDQYELKD 60
DB 1 MPRGMAAPLLLLLLGCGMGPDLVCTDYDTQTVICILEMNNLHPSTLTLTWQDQYELKD 60
QY 61 EATSCSLHRSANAHNATHTYTCMDVHFHMADDFSVNITDQSGVYSGECSFLAESIKP 120
DB 61 EATSCSLHRSANAHNATHTYTCMDVHFHMADDFSVNITDQSGVYSGECSFLAESIKP 120
QY 121 APPNNVTVTSSGQYNISWRSYEDPAFYMLKGKIQLEYLQYRNKDPMAVSPRRKLISVDS 180
DB 121 APPNNVTVTSSGQYNISWRSYEDPAFYMLKGKIQLEYLQYRNKDPMAVSPRRKLISVDS 180
QY 121 APPNNVTVTSSGQYNISWRSYEDPAFYMLKGKIQLEYLQYRNKDPMAVSPRRKLISVDS 180
DB 121 APPNNVTVTSSGQYNISWRSYEDPAFYMLKGKIQLEYLQYRNKDPMAVSPRRKLISVDS 180
QY 181 RSVSLPLERKDSYELQVRAGMPGSSYQGTWSEMSDPIVFTQOSEELKEGNNPHLL 240
DB 181 RSVSLPLERKDSYELQVRAGMPGSSYQGTWSEMSDPIVFTQOSEELKEGNNPHLL 240
QY 181 RSVSLPLERKDSYELQVRAGMPGSSYQGTWSEMSDPIVFTQOSEELKEGNNPHLL 240
DB 181 RSVSLPLERKDSYELQVRAGMPGSSYQGTWSEMSDPIVFTQOSEELKEGNNPHLL 240
QY 241 LLLLVIFIPAFMSLKTTHPLMKKIWAVPSPERFMPLYKGGSGDFKKVGAFTGSS 300
DB 241 LLLLVIFIPAFMSLKTTHPLMKKIWAVPSPERFMPLYKGGSGDFKKVGAFTGSS 300
QY 241 LLLLVIFIPAFMSLKTTHPLMKKIWAVPSPERFMPLYKGGSGDFKKVGAFTGSS 300
DB 241 LLLLVIFIPAFMSLKTTHPLMKKIWAVPSPERFMPLYKGGSGDFKKVGAFTGSS 300
QY 301 LEIGPMSPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVKPPSPFTAQNSSG 360
DB 301 LEIGPMSPEVSTLEVYSCHPPRSAPAKRLQTLQEPALVESDGVKPPSPFTAQNSSG 360
QY 361 SAYSEERDRPYGLVSIIDTVVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLJEDPLD 420
DB 361 SAYSEERDRPYGLVSIIDTVVLDAEGPCTWPCSCEDDGYPALDDAGLEBPGLJEDPLD 420
QY 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGDMAGGLPMWGRSPGVSESEAGS 480
DB 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGDMAGGLPMWGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGPOAS 538

RESULT 8
US-10-243-072-2
; Sequence 2, Application US/10243072
; Publication No. US20030148447A1
; GENERAL INFORMATION:

```

; APPLICANT: Preenell, Scott R.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US2003014844/Alak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55C1
; CURRENT APPLICATION NUMBER: US/10/243,072
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/628,127
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: US 09/404,641
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-072-2

Query Match      100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLILLLILQGGMGCPDLVCYTDYIQTIVCIEMNNLHPSLTLLTMOQDYEBELKD 60
Db 1 MPRGMAAPLILLLILQGGMGCPDLVCYTDYIQTIVCIEMNNLHPSLTLLTMOQDYEBELKD 60
QY 61 EATSCSLHRSANAHATATYTCMDVHFHMADDFSVNITDQSGVNSQECGSFLAESTIKP 120
Db 61 EATSCSLHRSANAHATATYTCMDVHFHMADDFSVNITDQSGVNSQECGSFLAESTIKP 120
QY 121 APPENVVTFTSGQYINISWRSDYEDPAFYMLKGKLYEQLQYRNKGDPMVAVSPRRKLISVDS 180
Db 121 APPENVVTFTSGQYINISWRSDYEDPAFYMLKGKLYEQLQYRNKGDPMVAVSPRRKLISVDS 180
QY 181 RSVSLLPLEFRKDSYELQVAPAGMPGSSYQGTWSEMSDPVIFQTQSEBELKEGNNPHLL 240
Db 181 RSVSLLPLEFRKDSYELQVAPAGMPGSSYQGTWSEMSDPVIFQTQSEBELKEGNNPHLL 240
QY 241 LLLIVIFIPAFMSLKTTHPLRLMKKIWA VPSPERFPMPLKYGSGDPFKKVVGA PFTGSS 300
Db 241 LLLIVIFIPAFMSLKTTHPLRLMKKIWA VPSPERFPMPLKYGSGDPFKKVVGA PFTGSS 300
QY 301 LELGPMSPPEVSTLEVYSCHPSPSPAKRLQUTELQEPALVESDGVKPSFMPPTAONSGG 360
Db 301 LELGPMSPPEVSTLEVYSCHPSPSPAKRLQUTELQEPALVESDGVKPSFMPPTAONSGG 360
QY 361 SAYSEERDRPYGLVSIOTVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBSPGLEDPLLD 420
Db 361 SAYSEERDRPYGLVSIOTVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBSPGLEDPLLD 420
QY 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGCVSESEAGS 480
Db 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGCVSESEAGS 480
QY 481 PLAGLMDTFTDSGFGVSDCSSPVECDFTSPGDBGPSPSYLRQWVVIPEPLSSPGPOAS 538
Db 481 PLAGLMDTFTDSGFGVSDCSSPVECDFTSPGDBGPSPSYLRQWVVIPEPLSSPGPOAS 538

RESULT 9
US-10-414-186-2
; Sequence 2, Application US/10414186
; Publication No. US20030175825A1
; GENERAL INFORMATION:
; APPLICANT: Preenell, Scott R.
```

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; APPLICANT: Conklin, Darrell C.
; APPLICANT: No. US20030175825A1ak, Julia E.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPLHA11
; FILE REFERENCE: 98-55
; CURRENT APPLICATION NUMBER: US/10/414,186
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/404,641
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-186-2

Query Match      100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2.8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLILLLILQGGMGCPDLVCYTDYIQTIVCIEMNNLHPSLTLLTMOQDYEBELKD 60
Db 1 MPRGMAAPLILLLILQGGMGCPDLVCYTDYIQTIVCIEMNNLHPSLTLLTMOQDYEBELKD 60
QY 61 EATSCSLHRSANAHATATYTCMDVHFHMADDFSVNITDQSGVNSQECGSFLAESTIKP 120
Db 61 EATSCSLHRSANAHATATYTCMDVHFHMADDFSVNITDQSGVNSQECGSFLAESTIKP 120
QY 121 APPENVVTFTSGQYINISWRSDYEDPAFYMLKGKLYEQLQYRNKGDPMVAVSPRRKLISVDS 180
Db 121 APPENVVTFTSGQYINISWRSDYEDPAFYMLKGKLYEQLQYRNKGDPMVAVSPRRKLISVDS 180
QY 181 RSVSLLPLEFRKDSYELQVAPAGMPGSSYQGTWSEMSDPVIFQTQSEBELKEGNNPHLL 240
Db 181 RSVSLLPLEFRKDSYELQVAPAGMPGSSYQGTWSEMSDPVIFQTQSEBELKEGNNPHLL 240
QY 241 LLLIVIFIPAFMSLKTTHPLRLMKKIWA VPSPERFPMPLKYGSGDPFKKVVGA PFTGSS 300
Db 241 LLLIVIFIPAFMSLKTTHPLRLMKKIWA VPSPERFPMPLKYGSGDPFKKVVGA PFTGSS 300
QY 301 LELGPMSPPEVSTLEVYSCHPSPSPAKRLQUTELQEPALVESDGVKPSFMPPTAONSGG 360
Db 301 LELGPMSPPEVSTLEVYSCHPSPSPAKRLQUTELQEPALVESDGVKPSFMPPTAONSGG 360
QY 361 SAYSEERDRPYGLVSIOTVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBSPGLEDPLLD 420
Db 361 SAYSEERDRPYGLVSIOTVTVLDAEGPCTWPCSCEDDGYPALDDAGLEBSPGLEDPLLD 420
QY 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGCVSESEAGS 480
Db 421 AGTTVLSGCGVSAAGSPGLGPGSLDLRLKPLADGEDMAGGLPMGGRSPGCVSESEAGS 480
QY 481 PLAGLMDTFTDSGFGVSDCSSPVECDFTSPGDBGPSPSYLRQWVVIPEPLSSPGPOAS 538
Db 481 PLAGLMDTFTDSGFGVSDCSSPVECDFTSPGDBGPSPSYLRQWVVIPEPLSSPGPOAS 538

RESULT 10
US-10-456-780-6
; Sequence 6, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
```

TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
FILE REFERENCE: 03-08
CURRENT APPLICATION NUMBER: US/10/456,780
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/387,127
PRIOR FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-10-456-780-6

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLILLLOGMCPCDLYCTDYIQTVCILEMNNLHPSLTTLTWODQYELKD 60
DB 1 MPRGMAAPLILLLOGMCPCDLYCTDYIQTVCILEMNNLHPSLTTLTWODQYELKD 60
QY 61 EATSCSLHRSANAHATATYTCNDVPHFMAADIFSVNITDQSGNYSQECGSFLLAESIKP 120
DB 61 EATSCSLHRSANAHATATYTCNDVPHFMAADIFSVNITDQSGNYSQECGSFLLAESIKP 120
QY 121 APPFNVTFTSGQYNISWRSYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
DB 121 APPFNVTFTSGQYNISWRSYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
QY 181 RSVSLPLERKSSYELQYRAGPMGSSYQGTWSEMSDPVIFQTQSEELKEGNPHLL 240
DB 181 RSVSLPLERKSSYELQYRAGPMGSSYQGTWSEMSDPVIFQTQSEELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTPLMLKKIWA VSPERFPMPLKYKCSGDFKMWGAPFTGSS 300
DB 241 LLLLVIFIPAFMSLKTPLMLKKIWA VSPERFPMPLKYKCSGDFKMWGAPFTGSS 300
QY 301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTELOEPAELVESDGVKPSFWPTAQNSSG 360
DB 301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTELOEPAELVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADGLESPGLEDDL 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADGLESPGLEDDL 420
QY 421 AGTTVLSGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGQAS 538
DB 481 PLAGLMDTDFDSGFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGQAS 538

RESULT 11
US-10-659-684-115
Sequence 115, Application US/10659684
Publication No. US20040110932A1
GENERAL INFORMATION:
APPLICANT: Novak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Grose, Jane A.
APPLICANT: Johnson, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/659,684

CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-10-659-684-115

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLILLLOGMCPCDLYCTDYIQTVCILEMNNLHPSLTTLTWODQYELKD 60
DB 1 MPRGMAAPLILLLOGMCPCDLYCTDYIQTVCILEMNNLHPSLTTLTWODQYELKD 60
QY 61 EATSCSLHRSANAHATATYTCNDVPHFMAADIFSVNITDQSGNYSQECGSFLLAESIKP 120
DB 61 EATSCSLHRSANAHATATYTCNDVPHFMAADIFSVNITDQSGNYSQECGSFLLAESIKP 120
QY 121 APPFNVTFTSGQYNISWRSYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
DB 121 APPFNVTFTSGQYNISWRSYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
QY 181 RSVSLPLERKSSYELQYRAGPMGSSYQGTWSEMSDPVIFQTQSEELKEGNPHLL 240
DB 181 RSVSLPLERKSSYELQYRAGPMGSSYQGTWSEMSDPVIFQTQSEELKEGNPHLL 240
QY 241 LLLLVIFIPAFMSLKTPLMLKKIWA VSPERFPMPLKYKCSGDFKMWGAPFTGSS 300
DB 241 LLLLVIFIPAFMSLKTPLMLKKIWA VSPERFPMPLKYKCSGDFKMWGAPFTGSS 300
QY 301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTELOEPAELVESDGVKPSFWPTAQNSSG 360
DB 301 LELGPMSPVSTLEVYSCHPPRSPAKRLQTELOEPAELVESDGVKPSFWPTAQNSSG 360
QY 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADGLESPGLEDDL 420
DB 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLADGLESPGLEDDL 420
QY 421 AGTTVLSGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
DB 421 AGTTVLSGCVSAGSPGLGPGLSLDRLKPLADGEDMAGGLPMGGRSPGVSESEAGS 480
QY 481 PLAGLMDTDFDSGFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGQAS 538
DB 481 PLAGLMDTDFDSGFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPLSSPGQAS 538

RESULT 12
US-10-620-169-4
Sequence 4, Application US/10620169
Publication No. US20040136954A1
GENERAL INFORMATION:
APPLICANT: Grunby, Michael J
APPLICANT: Wurster, Andrea
APPLICANT: Young, Deborah
APPLICANT: Collins, Mary
APPLICANT: Whittiers, Matthew
TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
FILE REFERENCE: 2205-565
CURRENT APPLICATION NUMBER: US/10/620,169
CURRENT FILING DATE: 2003-07-15

;; PRIOR APPLICATION NUMBER: 60/396,160
;; PRIOR FILING DATE: 2002-07-15
;; PRIOR APPLICATION NUMBER: 60/403,001
;; PRIOR FILING DATE: 2002-08-12
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 538
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-620-169-4

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLQGGGCPDLVCYTDYQTVICILEMNNLHPSTLTITMQDYEEELKD 60
DB 1 MPRGMAAPLLLLLLQGGGCPDLVCYTDYQTVICILEMNNLHPSTLTITMQDYEEELKD 60
QY 61 EATSCSLHRSANNAHTATYTCMDVFFHMAADIFSVNITDQSGNYSOECGSFLAESI KP 120
DB 61 EATSCSLHRSANNAHTATYTCMDVFFHMAADIFSVNITDQSGNYSOECGSFLAESI KP 120
QY 121 APPENVTVTSGQYNISMRSDYEDPAFYMLKGKLYEQLQRNRGDPMAVSPRRKLISYDS 180
DB 121 APPENVTVTSGQYNISMRSDYEDPAFYMLKGKLYEQLQRNRGDPMAVSPRRKLISYDS 180
QY 181 RSVSLPLERFKOSSYELQVRAGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNPHLL 240
DB 181 RSVSLPLERFKOSSYELQVRAGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNPHLL 240
QY 241 LLLIVIFIPAFMSLKTPLMLMKKIWA VSPERFPMPLKYKCGSDFKKVGA PFTGSS 300
DB 241 LLLIVIFIPAFMSLKTPLMLMKKIWA VSPERFPMPLKYKCGSDFKKVGA PFTGSS 300
QY 301 LEIGPMSPEVPSTLEVYSCHPPRS PAKRLQTELOEPAELVESDGVKPSFMPPTAONS GG 360
DB 301 LEIGPMSPEVPSTLEVYSCHPPRS PAKRLQTELOEPAELVESDGVKPSFMPPTAONS GG 360
QY 361 SAYSEERDRPYGLVSI DTVTYVLDAGPCTWPCSCEDDGPALDLDAGLEBPGLEDP LLD 420
DB 361 SAYSEERDRPYGLVSI DTVTYVLDAGPCTWPCSCEDDGPALDLDAGLEBPGLEDP LLD 420
QY 421 AGTTVLSGCGVSAGSPGLGSPGLSLDLRLKRPPLADGEDMAGCLPFGGRSPGCVSESEAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGSPGLSLDLRLKRPPLADGEDMAGCLPFGGRSPGCVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPOAS 538

RESULT 13
US-10-715-998-2
;; Sequence 2, Application US/10715998
;; Publication No. US20040204562A1
;; GENERAL INFORMATION:
;; APPLICANT: Prenell, Scott R.
;; APPLICANT: Conklin, Darrell C.
;; APPLICANT: Novak, Julia E.
;; APPLICANT: Hammond, Angela K.
;; TITLE OF INVENTION: CYTOKINE RECEPTOR ZAPPAH11
;; FILE REFERENCE: 98-55
;; CURRENT APPLICATION NUMBER: US/10/715,998
;; PRIOR FILING DATE: 2003-11-18
;; PRIOR APPLICATION NUMBER: US/10/414,186
;; PRIOR FILING DATE: 2003-04-14
;; PRIOR APPLICATION NUMBER: US/09/404,641
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/100,896
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,546

;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,574
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-06
;; NUMBER OF SEQ ID NOS: 91
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 2
;; LENGTH: 538
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-715-998-2

Query Match 100.0%; Score 2958; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRGMAAPLLLLLLQGGGCPDLVCYTDYQTVICILEMNNLHPSTLTITMQDYEEELKD 60
DB 1 MPRGMAAPLLLLLLQGGGCPDLVCYTDYQTVICILEMNNLHPSTLTITMQDYEEELKD 60
QY 61 EATSCSLHRSANNAHTATYTCMDVFFHMAADIFSVNITDQSGNYSOECGSFLAESI KP 120
DB 61 EATSCSLHRSANNAHTATYTCMDVFFHMAADIFSVNITDQSGNYSOECGSFLAESI KP 120
QY 121 APPENVTVTSGQYNISMRSDYEDPAFYMLKGKLYEQLQRNRGDPMAVSPRRKLISYDS 180
DB 121 APPENVTVTSGQYNISMRSDYEDPAFYMLKGKLYEQLQRNRGDPMAVSPRRKLISYDS 180
QY 181 RSVSLPLERFKOSSYELQVRAGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNPHLL 240
DB 181 RSVSLPLERFKOSSYELQVRAGMPGSSYQGTWSEMSDPVIFQTOSEELKEGNPHLL 240
QY 241 LLLIVIFIPAFMSLKTPLMLMKKIWA VSPERFPMPLKYKCGSDFKKVGA PFTGSS 300
DB 241 LLLIVIFIPAFMSLKTPLMLMKKIWA VSPERFPMPLKYKCGSDFKKVGA PFTGSS 300
QY 301 LEIGPMSPEVPSTLEVYSCHPPRS PAKRLQTELOEPAELVESDGVKPSFMPPTAONS GG 360
DB 301 LEIGPMSPEVPSTLEVYSCHPPRS PAKRLQTELOEPAELVESDGVKPSFMPPTAONS GG 360
QY 361 SAYSEERDRPYGLVSI DTVTYVLDAGPCTWPCSCEDDGPALDLDAGLEBPGLEDP LLD 420
DB 361 SAYSEERDRPYGLVSI DTVTYVLDAGPCTWPCSCEDDGPALDLDAGLEBPGLEDP LLD 420
QY 421 AGTTVLSGCGVSAGSPGLGSPGLSLDLRLKRPPLADGEDMAGCLPFGGRSPGCVSESEAGS 480
DB 421 AGTTVLSGCGVSAGSPGLGSPGLSLDLRLKRPPLADGEDMAGCLPFGGRSPGCVSESEAGS 480
QY 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPOAS 538
DB 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLRQWVVI PPPLSSPGPOAS 538

RESULT 14
US-10-872-087-2
;; Sequence 2, Application US/10872087
;; Publication No. US20040235743A1
;; GENERAL INFORMATION:
;; APPLICANT: Sprecher, Cindy A.
;; APPLICANT: Novak, Julia E.
;; APPLICANT: West, James W.
;; APPLICANT: Holli, Richard D.
;; APPLICANT: Nelson, Andrew J.
;; TITLE OF INVENTION: SOLUBLE ZAPPAH11 CYTOKINE RECEPTORS
;; FILE REFERENCE: 00-22D1
;; CURRENT APPLICATION NUMBER: US/10/872,087
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: US 60/194,731
;; PRIOR FILING DATE: 2000-04-05
;; PRIOR APPLICATION NUMBER: US 60/222,121
;; PRIOR FILING DATE: 2000-07-28
;; PRIOR APPLICATION NUMBER: US 09/825,561
;; PRIOR FILING DATE: 2001-04-03
;; NUMBER OF SEQ ID NOS: 86

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-10-872-087-2

Query Match 100.0%; Score 2958; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAAPLRLLLLOGGMGCPDLVCTDYQTVICILEMNNLHPSTLTLMQOYEBELKD 60
Db 1 MPRGMAAPLRLLLLOGGMGCPDLVCTDYQTVICILEMNNLHPSTLTLMQOYEBELKD 60
Qy 61 EATSCSLHRSANHATHTATYTCMDVPHFMADDFSVNITDQSGNYSQECGSLAESIKP 120
Db 61 EATSCSLHRSANHATHTATYTCMDVPHFMADDFSVNITDQSGNYSQECGSLAESIKP 120
Qy 121 APPNNVTTFSSGOYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
Db 121 APPNNVTTFSSGOYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
Qy 181 RSVSLPLERFKDSSYELQVRAGMPGSSYQGTWSEMSDVI FOTQSEELKEGNNPHLL 240
Db 181 RSVSLPLERFKDSSYELQVRAGMPGSSYQGTWSEMSDVI FOTQSEELKEGNNPHLL 240
Qy 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWAVSPERFEMPLYKCGSGDFKKWGAFTGSS 300
Db 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWAVSPERFEMPLYKCGSGDFKKWGAFTGSS 300
Qy 301 LELGPMSPPEVSTLEVYSCHPPRS PAKRLQLTLOEPAELVESDGVKPSFWPTAONSGG 360
Db 301 LELGPMSPPEVSTLEVYSCHPPRS PAKRLQLTLOEPAELVESDGVKPSFWPTAONSGG 360
Qy 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
Db 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
Qy 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
Db 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
Qy 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVI PPLSSPGPOAS 538
Db 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVI PPLSSPGPOAS 538

RESULT 15

US-10-787-442-115
Sequence 115, Application US/10787442
Publication No. US20040260065A1
GENERAL INFORMATION:
APPLICANT: Novak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/787,442
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11

PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
ORGANISM: Homo sapiens
US-10-787-442-115

Query Match 100.0%; Score 2958; DB 5; Length 538;
Best Local Similarity 100.0%; Pred. No. 2,8e-228;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRGMAAPLRLLLLOGGMGCPDLVCTDYQTVICILEMNNLHPSTLTLMQOYEBELKD 60
Db 1 MPRGMAAPLRLLLLOGGMGCPDLVCTDYQTVICILEMNNLHPSTLTLMQOYEBELKD 60
Qy 61 EATSCSLHRSANHATHTATYTCMDVPHFMADDFSVNITDQSGNYSQECGSLAESIKP 120
Db 61 EATSCSLHRSANHATHTATYTCMDVPHFMADDFSVNITDQSGNYSQECGSLAESIKP 120
Qy 121 APPNNVTTFSSGOYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
Db 121 APPNNVTTFSSGOYNISMRSDYEDPAFYMLKGLQYELQYRNKGDPMVAVSRRKLISVDS 180
Qy 181 RSVSLPLERFKDSSYELQVRAGMPGSSYQGTWSEMSDVI FOTQSEELKEGNNPHLL 240
Db 181 RSVSLPLERFKDSSYELQVRAGMPGSSYQGTWSEMSDVI FOTQSEELKEGNNPHLL 240
Qy 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWAVSPERFEMPLYKCGSGDFKKWGAFTGSS 300
Db 241 LLLLVIFIPAFMSLKTHTPLRLMKKIWAVSPERFEMPLYKCGSGDFKKWGAFTGSS 300
Qy 301 LELGPMSPPEVSTLEVYSCHPPRS PAKRLQLTLOEPAELVESDGVKPSFWPTAONSGG 360
Db 301 LELGPMSPPEVSTLEVYSCHPPRS PAKRLQLTLOEPAELVESDGVKPSFWPTAONSGG 360
Qy 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
Db 361 SAYSEERDRPYGLVSI DTVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDPILD 420
Qy 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
Db 421 AGTTVLSGCGVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
Qy 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVI PPLSSPGPOAS 538
Db 481 PLAGLMDTDFDSGFGVSDCSSPVECDFTSPGDEGPPRSYLQWVVI PPLSSPGPOAS 538

Search completed: September 7, 2006, 12:57:58
Job time : 197.717 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 12:53:56 ; Search time 33.0486 Seconds
(without alignments)
1143.601 Million cell updates/sec

Title: US-10-659-684-115

Perfect score: 2958
Sequence: 1 MPRGMAAPLLLLIQSGMGC.....YLQWVVIPLPPLSPGPQAS 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_CeJelerra_SIDS3/ptocdata/1/pubppaa/US09_NEW_PUB pep:*
- 2: /EMC_CeJelerra_SIDS3/ptocdata/1/pubppaa/US06_NEW_PUB pep:*
- 3: /EMC_CeJelerra_SIDS3/ptocdata/1/pubppaa/US07_NEW_PUB pep:*
- 4: /EMC_CeJelerra_SIDS3/ptocdata/1/pubppaa/US08_NEW_PUB pep:*
- 5: /EMC_CeJelerra_SIDS3/ptocdata/1/pubppaa/PC9 NEW_PUB pep:*
- 6: /EMC_CeJelerra_SIDS3/ptocdata/1/pubppaa/US10_NEW_PUB pep:*
- 7: /EMC_CeJelerra_SIDS3/ptocdata/1/pubppaa/US11_NEW_PUB pep:*
- 8: /EMC_CeJelerra_SIDS3/ptocdata/1/pubppaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2958	100.0	538	6 US-10-806-611-6	Sequence 6, Appli
2	2938	99.3	536	6 US-10-669-920-305	Sequence 305, App
3	2938	99.3	536	6 US-10-669-920-307	Sequence 307, App
4	1735.5	58.7	529	6 US-10-806-611-8	Sequence 8, Appli
5	1735.5	58.7	529	6 US-10-669-920-302	Sequence 302, App
6	284	9.6	549	6 US-10-669-920-285	Sequence 285, App
7	284	9.6	549	6 US-10-669-920-287	Sequence 287, App
8	240.5	8.1	537	6 US-10-669-920-280	Sequence 280, App
9	213	7.2	508	6 US-10-511-937-2426	Sequence 2426, Ap
10	213	7.2	890	6 US-10-669-920-292	Sequence 292, App
11	206	7.0	895	6 US-10-669-920-297	Sequence 297, App
12	206	7.0	895	6 US-10-669-920-299	Sequence 299, App
13	204.5	6.9	901	6 US-10-669-920-295	Sequence 295, App
14	193.5	6.5	825	6 US-10-505-928-650	Sequence 650, App
15	193.5	6.5	825	6 US-10-511-937-3001	Sequence 3001, Ap
16	192.5	6.5	819	6 US-10-669-920-523	Sequence 523, App
17	176	5.9	371	7 US-11-297-957-4	Sequence 4, Appli
18	176	5.9	371	7 US-11-344-379-4	Sequence 4, Appli
19	170.5	5.8	635	6 US-10-548-727-12	Sequence 12, Appli
20	168.5	5.7	635	6 US-10-511-937-2424	Sequence 2424, Ap
21	168.5	5.7	635	6 US-10-548-727-2	Sequence 2, Appli
22	168.5	5.7	635	6 US-10-548-727-4	Sequence 4, Appli
23	168.5	5.7	635	6 US-10-548-727-10	Sequence 10, Appli
24	151	5.1	457	6 US-10-669-920-1240	Sequence 1240, Ap
25	150.5	5.1	501	6 US-10-548-727-6	Sequence 6, Appli

26	146	4.9	459	6 US-10-511-937-2465	Sequence 2465, Ap
27	146	4.9	459	7 US-11-297-957-2	Sequence 2, Appli
28	146	4.8	369	6 US-10-511-937-2966	Sequence 2966, Ap
29	137	4.6	953	7 US-11-312-958-56	Sequence 56, Appli
30	127	4.3	1012	6 US-10-519-342-3	Sequence 3, Appli
31	123	4.2	464	6 US-10-669-920-1407	Sequence 1407, Ap
32	118.5	4.0	613	6 US-10-669-920-520	Sequence 520, Appli
33	117.5	4.0	500	7 US-11-194-051-22	Sequence 22, Appli
34	117.5	4.0	577	7 US-11-194-051-23	Sequence 23, Appli
35	117.5	4.0	1460	7 US-11-247-437-14	Sequence 14, Appli
36	117	4.0	422	7 US-11-296-092-32	Sequence 32, Appli
37	117	4.0	422	7 US-11-296-155-32	Sequence 32, Appli
38	117	4.0	422	7 US-11-300-928-27	Sequence 27, Appli
39	117	4.0	836	6 US-10-511-937-2988	Sequence 2988, Ap
40	117	4.0	836	7 US-11-313-104-16	Sequence 16, Appli
41	114.5	3.9	581	6 US-10-953-349-32682	Sequence 32682, A
42	114.5	3.9	581	7 US-11-056-355B-64207	Sequence 64207, A
43	114.5	3.9	594	6 US-10-953-349-32681	Sequence 32681, A
44	114.5	3.9	594	7 US-11-056-355B-64206	Sequence 64206, A
45	112.5	3.8	638	7 US-11-314-257-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-806-611-6
; Sequence 6, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chin, Elaine Y.
; APPLICANT: Senice, Mayra
; APPLICANT: Young, Deborah A.
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
; TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
; FILE REFERENCE: 16158-013001
; CURRENT APPLICATION NUMBER: US/10/806, 611
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 60/456,920
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-611-6

QY	1	MPRMAAPLLLLLLIQSGMGC	100.0%; Score 2958; DB 6; Length 538;
QY	1	MPRMAAPLLLLLLIQSGMGC	Best Local Similarity 100.0%; Pred. No. 1.7e-231;
DB	1	MPRMAAPLLLLLLIQSGMGC	Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MPRMAAPLLLLLLIQSGMGC	Sequence 6, Appli
DB	1	MPRMAAPLLLLLLIQSGMGC	Sequence 6, Appli
QY	61	EATCSLHRSANHTATYTCTHMDVHFHMADISVNTTDSGNYSGOEGSFLAESTIKP	Sequence 305, App
DB	61	EATCSLHRSANHTATYTCTHMDVHFHMADISVNTTDSGNYSGOEGSFLAESTIKP	Sequence 305, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 307, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 307, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 8, Appli
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 8, Appli
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 302, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 302, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 285, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 285, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 287, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 287, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 280, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 280, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 2426, Ap
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 2426, Ap
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 292, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 292, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 297, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 297, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 299, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 299, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 295, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 295, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 650, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 650, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 3001, Ap
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 3001, Ap
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 523, App
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 523, App
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 4, Appli
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 4, Appli
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 4, Appli
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 4, Appli
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 10, Appli
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 10, Appli
QY	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 1240, Ap
DB	121	APPNNVTTFSGQYNISWRSYEDPAPFMYLKGKQYELQYRNKRDPMVAVSRRKLI	Sequence 1240, Ap

```
Qy 301 LEIGPWSPEVPSSTLEVYVSCHPRRSPAKRLQLTLEQEPALVEVDGVKPSFWPTAQNSSG 360
Db 301 LEIGPWSPEVPSSTLEVYVSCHPRRSPAKRLQLTLEQEPALVEVDGVKPSFWPTAQNSSG 360
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLLD 420
Db 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLLD 420
Qy 421 AGTTVLSGCCVVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
Db 421 AGTTVLSGCCVVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
Qy 481 PLAGLMDTDFDGSFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPQAS 538
Db 481 PLAGLMDTDFDGSFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPQAS 538

RESULT 2
US-10-669-920-305
; Sequence 305, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moritz, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-305

Query Match 99.3%; Score 2938; DB 6; Length 536;
Best Local Similarity 99.6%; Pred. No. 7.2e-230;
Matches 536; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
```

```
Db 239 LLLLVIFIPAFWSLTKNHLPLRLWKKIWAVPSEPFMPLYKGGSGDFKKNVGAAPFGSS 298
Qy 301 LEIGPWSPEVPSSTLEVYVSCHPRRSPAKRLQLTLEQEPALVEVDGVKPSFWPTAQNSSG 360
Db 299 LEIGPWSPEVPSSTLEVYVSCHPRRSPAKRLQLTLEQEPALVEVDGVKPSFWPTAQNSSG 358
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLLD 420
Db 359 SAYSEERDRPYGLVSDITVTVLDAEGPCTWPCSCEDDGYPALDLDAGLESPGLEDDPLLD 418
Qy 421 AGTTVLSGCCVVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 480
Db 419 AGTTVLSGCCVVSAGSPGLGPGSLDLRLKPLADGEDMAGGLPWGGRSPGVSESEBAGS 478
Qy 481 PLAGLMDTDFDGSFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPQAS 538
Db 479 PLAGLMDTDFDGSFVSDCSSPVECDFTSPGDEGPPRSYLRQWVVIIPPPLSSPGPQAS 536

RESULT 3
US-10-669-920-307
; Sequence 307, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moritz, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 307
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-307

Query Match 99.3%; Score 2938; DB 6; Length 536;
Best Local Similarity 99.6%; Pred. No. 7.2e-230;
Matches 536; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
```

Db 179 RSVSLPLFERKDSYELQVRAGPMGSSYQGTWSEMSDPIVIFOTOSBBLKEGMNPHLL 238
Qy 241 LLLLVVIFPAFWSLKTHPMLRMKTIWAPSPERFPMPIYKCGSGDFKKWCAPFPGSS 300
Db 239 LLLLVVIFPAFWSLKTHPMLRMKTIWAPSPERFPMPIYKCGSGDFKKWCAPFPGSS 298
Qy 301 LELGPMSPVSTLEYVSCPPRSPAKRLQTELOEPAELVESDGVKPSFMTAQNCG 360
Db 299 LELGPMSPVSTLEYVSCPPRSPAKRLQTELOEPAELVESDGVKPSFMTAQNCG 358
Qy 361 SAYSEERDRPYGLVSDITVTVLDAEGPCITWPCSCEDDGYPALDLADGLBPSPGLEDL 420
Db 359 SAYSEERDRPYGLVSDITVTVLDAEGPCITWPCSCEDDGYPALDLADGLBPSPGLEDL 418
Qy 421 AGTTVASCVCVSGSPGLGPGSLDLRLKPLADGDMAGGLPMGGRSPGVSESGS 480
Db 419 AGTTVASCVCVSGSPGLGPGSLDLRLKPLADGDMAGGLPMGGRSPGVSESGS 478
Qy 481 PLAGLMDTFDSDGVSGSDCSSPVCECDFTSPGDEGPPRSYLROWVILPPILSPQOAS 538
Db 479 PLAGLMDTFDSDGVSGSDCSSPVCECDFTSPGDEGPPRSYLROWVILPPILSPQOAS 536

RESULT 4

US-10-806-611-8
; Sequence 8, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chin, Elaine Y.
; APPLICANT: Senices, Mayra
; APPLICANT: Young, Deborah A.
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING ACONISTS OF
; FILE REFERENCE: 16158-013001
; CURRENT APPLICATION NUMBER: US/10/806,611
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 60/456,920
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent version 3.2
; SEQ ID NO 8
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-806-611-8

Query Match 58.7%; Score 1735.5; DB 6; Length 529;

Best Local Similarity 62.7%; Pred. No. 1.6e-132; Indels 17; Gaps 6;
Matches 340; Conservative 49; Mismatches 136;

Qy 1 MPRGMAAPLLLLLLLOGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTMODOYEBLKD 60
Db 1 MPRGMAAPLLLLLLLOGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTMODOYEBLKD 60
Qy 61 EATSCSLHRSANAHATATYTCMDVFHFMADDIFSVNITDQSGNYSQECGSFLAIESIKP 120
Db 61 EATSCSLHRSANAHATATYTCMDVFHFMADDIFSVNITDQSGNYSQECGSFLAIESIKP 120
Qy 121 APPENVTVTSSGQYNISWSDYEDPAFYMKGLQYELQVRNKGDPMAVSPRKLISVDS 180
Db 121 APPENVTVTSSGQYNISWSDYEDPAFYMKGLQYELQVRNKGDPMAVSPRKLISVDS 180
Qy 121 APPENVTVTSSGQYNISWSDYEDPAFYMKGLQYELQVRNKGDPMAVSPRKLISVDS 180
Db 121 APPENVTVTSSGQYNISWSDYEDPAFYMKGLQYELQVRNKGDPMAVSPRKLISVDS 180
Qy 181 RSVSLPLFERKDSYELQVRAGPMGSSYQGTWSEMSDPIVIFOTOSBBLKEGMNPHLL 240
Db 181 RSVSLPLFERKDSYELQVRAGPMGSSYQGTWSEMSDPIVIFOTOSBBLKEGMNPHLL 240
Qy 241 LLLLVVIFPAFWSLKTHPMLRMKTIWAPSPERFPMPIYKCGSGDFKKWCAPFPGSS 299
Db 241 LLLLVVIFPAFWSLKTHPMLRMKTIWAPSPERFPMPIYKCGSGDFKKWCAPFPGSS 299
Qy 300 SLELGPMSPVSTLEYVSCPPRSPAKRLQTELOEPAELVESDGVKPSFMTAQNCG 356
Db 300 SLELGPMSPVSTLEYVSCPPRSPAKRLQTELOEPAELVESDGVKPSFMTAQNCG 356

Db 300 SLELVQSSITTSAL-----HSLYPAKEKKEFPGLGLEOLECDGMSPEGHWCITPLAA 354
Qy 357 NSGGSAYSEERDRPYGLVSDITVTVLDAEGPCITWPCSCEDDGYPALDLADGLBPSPGLE 416
Db 355 GQAVSAYSEERDRPYGLVSDITVTVLDAEGPCITWPCSCEDDGYPALDLADGLBPSPGLE 414
Qy 417 PLUDACTVLSGCVSAGSPGLGPGSLDLRLKPLADGDMAGGLPMGGRSPGVSESGS 476
Db 415 LLLVTPAPFLSCGCVSGSGSLRLGSGSPGSLDLRLKPLADGDMAGGLPMGGRSPGVSESGS 474
Qy 477 EAGSPPLAGLMDTFDSDGVSGSDCSSPVCECDFTSPGDEGPPRSYLROWVILPPILSPQO 536
Db 475 EAGSP-PLGMDTFDSDGVSGSDCSSPVCECDFTSPGDEGPPRSYLROWVILPPILSPQO 527
Qy 537 AS 538
Db 528 SS 529

RESULT 5

US-10-669-920-302
; Sequence 302, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-669-920-302

Query Match 58.7%; Score 1735.5; DB 6; Length 579;

Best Local Similarity 62.7%; Pred. No. 1.6e-132; Indels 17; Gaps 6;
Matches 340; Conservative 49; Mismatches 136;

Qy 1 MPRGMAAPLLLLLLLOGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTMODOYEBLKD 60
Db 1 MPRGMAAPLLLLLLLOGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTMODOYEBLKD 60
Qy 51 MPRGMAAPLLLLLLLOGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTMODOYEBLKD 110
Db 51 MPRGMAAPLLLLLLLOGMGCPDLVCYTDYQTVICILEMNNLHPSTLTLTMODOYEBLKD 110
Qy 61 EATSCSLHRSANAHATATYTCMDVFHFMADDIFSVNITDQSGNYSQECGSFLAIESIKP 120
Db 61 EATSCSLHRSANAHATATYTCMDVFHFMADDIFSVNITDQSGNYSQECGSFLAIESIKP 120
Qy 111 EATSCSLHRSANAHATATYTCMDVFHFMADDIFSVNITDQSGNYSQECGSFLAIESIKP 170
Db 111 EATSCSLHRSANAHATATYTCMDVFHFMADDIFSVNITDQSGNYSQECGSFLAIESIKP 170
Qy 121 APPENVTVTSSGQYNISWSDYEDPAFYMKGLQYELQVRNKGDPMAVSPRKLISVDS 180
Db 121 APPENVTVTSSGQYNISWSDYEDPAFYMKGLQYELQVRNKGDPMAVSPRKLISVDS 180
Qy 171 APPENVTVTSSGQYNISWSDYEDPAFYMKGLQYELQVRNKGDPMAVSPRKLISVDS 230
Db 171 APPENVTVTSSGQYNISWSDYEDPAFYMKGLQYELQVRNKGDPMAVSPRKLISVDS 230
Qy 181 RSVSLPLFERKDSYELQVRAGPMGSSYQGTWSEMSDPIVIFOTOSBBLKEGMNPHLL 240
Db 181 RSVSLPLFERKDSYELQVRAGPMGSSYQGTWSEMSDPIVIFOTOSBBLKEGMNPHLL 240
Qy 231 RSVSLPLFERKDSYELQVRAGPMGSSYQGTWSEMSDPIVIFOTOSBBLKEGMNPHLL 290
Db 231 RSVSLPLFERKDSYELQVRAGPMGSSYQGTWSEMSDPIVIFOTOSBBLKEGMNPHLL 290

```
Qy 241 LLLVIVIPAFMELKTHPLRLMKIWA-VSPERFPMPLKGCSDGDFKKVGAFTGS 299
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 291 LLAVALIIVL-VFMGLKTHLPRLMKIWAIPVTPESFPQPIRHSNGFKMVAITPFTAS 349
Qy 300 SLELPMSPPEVPSLTLEVYSCHPPSPAKRLQTLQEPALVESDGVKPSFM---PTAQ 356
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 350 SIELVPSSTTSLA-----HLISLYPAKEKFKPGLPGLAEQLECDGMEHPCHWCIPLAA 404
Qy 357 NSGSAVSEERDRYGLVSTITVTVLDAEGCTPCCSEDDGYPALDDALLESFGLD 416
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 405 GQAVSAVSEERDRYGLVSTITVTVGDAEGLCVWPCSCEDDGYPAMNLDAGRESGPNSED 464
Qy 417 PLLDAGTTVSCGCVSAGSPGLGSLDRKLPPLADGEDMAGLPMWGRSPGVSES 476
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 465 LLLVTDAPFASCGCVSAGSLRGLSGPSLLDRKLSPAKEDMTADPTWRGSPGSGSES 524
Qy 477 EAGSPLAGLMDTDFSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVVIPLPLSPGPQ 536
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 525 EAGSP-FGLMDTDFSGFVSGDCSSPVECDFTSPGDEGPPRSYLROWVVIPLPLSPGPQ 577
Qy 537 AS 538
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 578 SS 579

RESULT 6
US-10-669-920-285
; Sequence 285, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moritz, David W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-285
```

```
Query Match 9.6%; Score 284; DB 6; Length 549;
Best Local Similarity 26.1%; Pred. No. 5.6e-15;
Matches 137; Conservative 73; Mismatches 201; Indels 114; Gaps 30;
```

```
Qy 5 WAAPLILL--LOGG-----GCPDLYCYTDYLGQVYICLEMNNLHPSTLTITWQOYE 56
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 8 WRPLILLPLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS-----ODG 52
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 57 ELKDEATSCSLH-----RSANNA-----HATYTCM-----DVHFMAADIFSUNITD 100
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 53 ALQD--TSCQVHAMPRDRRNNGTCELLPVSQASWACNLLIGAPDSQKLTITVDITLVLC 110
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
```

```
Qy 101 QSGNYSQECG--SFLAESIKPAPFENVTVTFSGQVYNISNRSDYEDPAFYMLKGLQYEL 158
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 111 REGVRRMVAALIQPKPENRLMAPISLQVHVETCNISWEI---SQASHYFERHLEFEA 167
Qy 159 QYRNQDPAVSPRRKLISVDSRSVSLPLPEFRKDSSEYELQVAGPMPGSSYOGTSEMS 218
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 168 RTLSPGHTWEAP---LLTLKQOEWCLETLTPDTQYERQVAVKPLQGEF---TWSFMS 222
Qy 219 DPAVFOGSEBELKGG---KNPHTLLLLVIVFIPAFMSL-----KTHPLRLM-KKIWA- 269
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 223 QPLAFRTKPPALGKDTIIPWGLHLLVLSGAFGIILVYLINCRNP-----MLKVLKC 278
Qy 270 -VSPERFPMPLKGCSDGDFKKVGAFTGSLSLELGMSPPEVPSLTLEVYSCHPPSPAKR 328
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 279 NTPDPSKFFSQLSSEHGDVQXWLSFPSSSPGLADEI-SPLEV-----LER 328
Qy 329 LQTLQEPALVESDGVKPSFMPTAQNQSGSAVSEERDRYGLVSTITVTVLDAEGPC 388
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 329 DKYTQL-----LQODKVPPEPA-----SLSNHSLTSCFTQGYFFPHLPALIEIA---C 376
Qy 389 -----TWPCGEDD-----GYPALDDAGLEPSPGLEPPLDAGTTVLSGCVSAGSPG- 437
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 377 QVYFTYDPISEEDPDEGACAPFGSSFPQPLQSLG-BD---DAYCTFSPSDLLILFSPSL 432
Qy 438 LGGP-----LGSLLDRKLPPLAD--CEDWAGLPMWGRSPG 471
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 433 LGGPSPSTAPGSGAGGERMPPSLQERVRDW-DPQPLGPPPTG 476
```

```
RESULT 7
US-10-669-920-287
; Sequence 287, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moritz, David W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 287
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-287
```

```
Query Match 9.6%; Score 284; DB 6; Length 549;
Best Local Similarity 26.1%; Pred. No. 5.6e-15;
Matches 137; Conservative 73; Mismatches 201; Indels 114; Gaps 30;
```

```
Qy 5 WAAPLILL--LOGG-----GCPDLYCYTDYLGQVYICLEMNNLHPSTLTITWQOYE 56
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 8 WRPLILLPLPLATSWASAAVNGTSQFTCFYNSRANISCV---WS-----ODG 52
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 57 ELKDEATSCSLH-----RSANNA-----HATYTCM-----DVHFMAADIFSUNITD 100
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
```

```

Db      53 ALDD--TSCOVHAMPDRRNQTCCELLPVSOASMACNLLIAPDSOKLTTVDITLAVLC 110
Qy      101 QSGNYSQECG--SFLAESIKPAPFNVVTFSCQYNI SMRSYEDBAFTWLKGLQYEL 158
Db      111 REGVRAVMAIQDPKPFENLRMAPISLOVHVETCISWEI---SQASHYFERHLEFEA 167
Qy      159 QYRRGDPMAVSPRRKLI SVDSRSVSLPLEFRKDSYELQYRAGPMGSSYQGTSEMS 218
Db      168 RTISPGHTWEAP---LTLTKQKQEWI CLETLTPDTQYEFQVRKPLQGER--TTWSPWS 222
Qy      219 DPVIFQOSEELKXG---WNPMLLLLVLVFI PAFMSL---KTHPLRLM--KXIMA- 269
Db      223 QPLAFKRPALGKDTTPMIGHLVLVSGARGFIILVYLINCNTGP---WLKXVLC 278
Qy      270 -VSPERPFMPLYKSGSGDFKKWVGAPFTGSSLELGWSPBPSTLEVYSGHPPSPAKR 328
Db      279 NTPDPSKFFSGLSEHGSDVQKWLSPSSPSSFGGLAPEI-SPLEV-----LER 328
Qy      329 LQTLLEAPALVESDGVPKPSFWPTNONGSGSAYSEBRPYGLVSDITVTLDAAGPC 388
Db      329 DKYTL-----LLOQDKVPEPA---SLSSNHSILTSCFTNQGYPFPHLPDALEIEA---C 376
Qy      389 -----TWPCSGEDD-----GYPALDLDAGLEPSPGLEPDLDACTVLSGCGVAGSPG- 437
Db      377 QYVFTYDPIYSEBDEGVAGAFPTGSSPOLOPLSG-BD---DAYCTPSPRDDLLFSPSL 432
Qy      438 LGSP-----LGSLLDLRLKPLAD--GEDWAGLPMGGRSPG 471
Db      433 LGGSPSPSTAPGSGAGEBRMPPLQGRVPRDW-DPQLPGRPTG 476

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RESULT 8 US-10-669-920-280

```

; Sequence 280, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Moritz, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004, 113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052, 482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997, 722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034, 650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085, 117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087, 192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322, 281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322, 696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-669-920-280

```

Query Match 8.1%; Score 240.5; DB 6; Length 537;
Best Local Similarity 23.6%; Pred. No. 1.8e-11;
Matches 138; Conservative 64; Mismatches 198; Indels 185; Gaps 30;

Qy 5 WAAPL--LILLGSGW-----GCPDLVCTDVTQYTCLEMMNLHPSLTTLTWQOYE 56

```

Db      8 WSLVLYELLLATPMAAIVKNOCSHLECFYNSRANVSC---MWS-HEBALNV----- 56
Qy      57 ELKDEATSCGLHSAHNAATATYTCMDVPH-----EMADIFPSVNI 98
Db      57 -----TTCVHAKS-NLRHMNKTCELLVROASMACNLLIGSPESQSLTSVLLINV 109
Qy      99 T--DQSGNYSQECGSLAESIKPAPFNVVTF--SGQYNISWR-----SDYEDPAFTYL 150
Db      110 VCBEKGMRRVKTCDFHPFNLRVAPHSLOVHLIDTQRCNISKVSVSHYIEP----- 164
Qy      151 KGLQYELQYRRNGDPMAVSPRRKLI SVDSRSVSLPLEFRKDSYELQYRAGPMGSSY 210
Db      165 --YLEFARRRLIGHSEDA---SVLSKQRQOMLFEMLI PSTSYEQYRVKAKRANT- 218
Qy      211 QGTWSEKSDPVITQ---TQSEELKEGNPHLLLVLVYFI PAFMS----- 254
Db      219 -GTWSPWSQLTRFMDPMKEIILPMWS---LRYLLVLVLCFSGFSCVYILVKRYLGP 273
Qy      255 -----LKTHPLRLMKKIWAVSPERPFMPLYKSGSGDFKKWVGAPFTGSSLELGPMSP 309
Db      274 WLKTVLKC-----IPDSEFFSGLSSOHGDLQKWLSSPVLSFPSPGPAPE 322
Qy      310 VPSTLEVYSGHPPSPAKRLQTLLEAPALVESDGVPKPSFWPTNONGSGSAYSEBRDR 369
Db      323 I-SPLVLD-----GOSKAVQL-----LLOKDSAPLS-----PSGHSQASCTNQ 363
Qy      370 PY-----GLVSDITVTLDAEGPCT-----WPCSGEDDGY----- 399
Db      364 GYFFPHLPNALETIESCQVFTYDPCVBEVEEDGSRLEPSPPLPLPGLGEBODDYCAFP 423
Qy      400 PALDLDAGLEPSPGLEPDLDACTT-----VLSGCVASGSPGLGSLDLRLK 450
Db      424 PRDDL---LIFSPLSTPNTAYGSRAPBERSPLSLHGLPLSARLDMG-LQRPLERM- 478
Qy      451 PPLADGEDWAGLPMGGRSPGVSESEAGSP-----LAGLPMID 488
Db      479 -PEGDGE-----GLSANSGEQASVPEGNLHGQDD 508

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RESULT 9

```

US-10-511-937-2426
; Sequence 2426, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fey, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Moritz, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511, 937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131, 831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325, 899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2426
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2426

```

Query Match 7.2%; Score 213; DB 6; Length 508;
Best Local Similarity 21.6%; Pred. No. 2.9e-09;

Qy 5 WAAPL--LILLGSGW-----GCPDLVCTDVTQYTCLEMMNLHPSLTTLTWQOYE 56

	Matches	127;	Conservative	63;	Mismatches	175;	Indels	224;	Gaps	30
OY	9	L L L L L L O G W C P R	-----	-----	D V C T D Y L Q V I C L E	--	M N L H P	44		
Db	15	L C L L A G A M A P P N U L P D K F E S K A A L L A A R P E E L C F T E R L E D L C W B E A A S A G V P R	----	----	: : : : : : : : : : : :		:	74		
OY	45	S T L T L W O D Q Y E L K D E A T S - C S L R S A H N A T H A Y T T C M --	---	---	D Y F H F A A D D I F S V N I T D			100		
Db	75	G N Y S S Y Q ----- L E D E P K L C R L H O A P R A R G A N R F W C S L P A D I S S F V P ---	---	---	L E I R Y T A		:	126		
OY	101	O S G N Y S O E C S F L A E S I K P A P P F V N Y T F	-----	-----	S G O Y N I S W R S D		141			
Db	127	A S G -----	---	---	A P R Y H R V I H I N E V L L D A P V G L V A R L A D E S G H V I R M L P P		169			
OY	142	Y E D P A F Y M L K G L Q Y E L Q Y R N R G D P M A S P R K K I S V D S R S Y L P L E R K O S S Y E L O Y R	201							
Db	170	P E T P --- M T S H I R Y E V D V S A G N G A S V --	---	---	O R V E L E R T E C V L S - N L R G R T Y T F A V R		221			
OY	202	A G P M P G S S Y O G W S E M S D P V I F Q T O S E E L K E G M P H L L -	---	---	L L L Y I V I P A F W S L K T H P		259			
Db	222	A - R M A P E S T G G W S A N S E P V S L T T S D ---	---	---	L D P L I L T S L I V I L V I L L V L L A L L S H R		275			
OY	260	I M R L W K I W - A Y P S E R F F M P L Y K G C S G D P K K V ---	---	---	G A P E T G S L E L G P M S P E V P S T L		314			
Db	276	R - A L N Q K I M P G I P S P E S E F E G L F T T H K G F Q L M L Q N O C L W ---	---	---	W S P C P F T E		325			
OY	315	E V Y S C H P P R S P A K R L Q L E T E L Q P A E L V E S D G V P K S F W F T A O N S G S A Y S E R D R Y G L V	374							
Db	326	D --- P P A S ---	---	---	L E V L S E R C ---	---	W G T W O ---	343		
OY	375	S I D T Y T V I D A E G P C T M P C S C E D D Y P A L D L D A G L E P S P L E D P L D A G T T V L S C G S V A G	434							
Db	344	A E P E G T - D D E G P L L E P V G S E H A O T Y T L V L D K W L P R	-----	-----			378			
OY	435	S P G L G P L G S L L D R L K P L A D E D W A G C L P M G R S P G G V S E S E A G S P L A G L M D T F D S G F	494							
Db	379	-----	---	---	N P S E D ---	---	L P ---	G P G S ---	S V D I V A M D B S S	401
OY	495	V G S D C S S P V E C D F T S P G D E G ---	---	---	P P R S Y L R Q M V I P -	PP	529			
Db	402	E A S S C S S A L A ---	---	---	S K R S P E G A S A S E F Y T I L D P S Q L R P W L C E L P P		447			
	RESULT 10									
	US-10-669-920-292									
	; Sequence 292, Application US/10669920									
	; Publication No. US20060194265A1									
	; GENERAL INFORMATION:									
	; APPLICANT: Morris, David W.									
	; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER									
	; FILE REFERENCE: 20366-066001									
	; CURRENT APPLICATION NUMBER: US/10/669,920									
	; CURRENT FILING DATE: 2003-09-23									
	; PRIOR APPLICATION NUMBER: US 10/004,113									
	; PRIOR FILING DATE: 2001-10-23									
	; PRIOR APPLICATION NUMBER: US 10/052,482									
	; PRIOR FILING DATE: 2001-11-08									
	; PRIOR APPLICATION NUMBER: US 09/997,722									
	; PRIOR FILING DATE: 2001-11-30									
	; PRIOR APPLICATION NUMBER: US 10/034,650									
	; PRIOR FILING DATE: 2001-12-20									
	; PRIOR APPLICATION NUMBER: US 10/085,117									
	; PRIOR FILING DATE: 2002-02-27									
	; PRIOR APPLICATION NUMBER: US 10/087,192									
	; PRIOR FILING DATE: 2002-03-01									
	; PRIOR APPLICATION NUMBER: US 10/322,281									
	; PRIOR FILING DATE: 2002-12-17									
	; PRIOR APPLICATION NUMBER: US 10/322,696									
	; PRIOR FILING DATE: 2002-12-17									
	; NUMBER OF SEQ ID NOS: 1441									
	; SOFTWARE: FaastSD for Windows Version 4.0									

```

; LENGTH: 890
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-669-920-292

Query Match      7.2%; Score 213; DB 6; Length 890;
Best Local Similarity 20.3%; Pred. No. 5.9e-09;
Matches 112; Conservative 84; Mismatches 221; Indels 136; Gaps 24

OY 22 DLVCTYDYLQVNTLILEMNN-----LHSTLTLLTWQDQYELKEDEATSCSLRS 70
Db 248 NLQCFPGIOGSLHCSWEWVQTGTSVSFGLFYRBSPTA-----PEEKCSFVVER 297
OY 71 AHNATHTATYTCNMVDFHFHMADDFSVNTITDQSGVNSQEGSFLLA-ESIKPAP-FNYTV 128
Db 298 PGASVYTRHYKSLFLVPEPSAHSQYTVSK-----HLEQGFIMSYNHIOHEPFLNLTK 351
OY 129 TFGQYINISWRSDYEDPAFYMLKKGLOELOYLRNRGDMAVSPRRKLISVDSRSVSLPL 188
Db 352 N-RDYSYLHWETQWMAYSFI-----EHFTQVQYKKKSDMEDSKTENLDRAHSMDS---- 402
OY 189 EFRKDSSEYELQYRGRPMBSGYOQTWSHMSDPVIFQTOSEELKEGMNPHLLLLLVYVF 248
Db 403 QLEPDTSYCARVRKPI--SNYDGIWSKMSSEETWKT-DWVMPTLIVLILVFLITLTL 459
OY 249 IIPAFMSLKTPIHMLMKIMAVNPPERPFMWLYKCGSGDFPKMWGA-PTGSSLELGPMSP 308
Db 460 IIRFGCVSVRY--KWE-KIPNPSKSL-----FQDGKGLMP--- 495
OY 309 EVESTLELYVSGHP--RSPAKRLQLTLEQBAELVESDGVKPSFWPTAONSGSAYSEE 366
Db 496 --PSSMAFAIKNPALQGPQSRLL-LAEQ-----GESYHL 528
OY 367 RDRPYGLVSDITVTVL--DAEGPCTWPCSCD--DGYPALDLADLGSFGLIEDLUDAG 422
Db 529 EDNNVSPLTIEDPIIRVPSPGPTTPPAASSESTQELPNVQVEGPTPRPKQLSPFD-- 586
OY 423 TTVLSCGVASGSGTGLGP-----IGSLIDRLKPLADE---DMAAGLPMWGRSPGCG-- 472
Db 587 -----FNGYLPGRPOHSLPLDLPDQGSFVYGSGLKPALPGSLFYMKLPRGGCAQ 636
OY 473 -----VSESEAGSPLAGLMDPTFDGSGFVGSDCSSPYECDFTSBGDEGPPRSYLROWV 525
Db 637 LVPLSQWVGCGQANDVQCGSLETFSGSVAPKEMPVFLSMIEQEARNDP----- 687
OY 526 IPPPLSSBPQAS 538
Db 688 VTLPISSGPEGS 700

RESULT 11
US-10-669-920-297
; Sequence 297, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01

```


PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 297
LENGTH: 895
TYPE: PRT
ORGANISM: Homo sapiens
US-10-669-920-297

Query Match 7.0%; Score 206; DB 6; Length 895;
Best Local Similarity 22.9%; Pred. No. 2.2e-08;
Matches 142; Conservative 66; Mismatches 225; Indels 188; Gaps 31;

QY 22 DLVCTDYLTQVTCILEMMNLHPSTLT-LTWODYBELKDEATSC-----SLHSAH- 72
DB 245 NLECFPGGAVALSCSWEKREKVASVSFGLFYKPSPDAGEBEGSPVLRGLSLHTRHHC 304
QY 73 -----NATATYTCCHMDVFHFMAADIFSVNITQSGNYSQECGSLIAESIKAPPPNV 126
DB 305 QIPVPDPATHGQY-----IVSV-----QPRRAEKHKS---SVNIQMAPP-SL 343
QY 127 TWTFSG-QYNISW-----RSDYEDPAFYMLKGKLOLEYQYNNRGDPMASPRKLIYSVS 180
DB 344 NVTKDGSYSILRWETMKRYEHIDHTF-----EIQYKDDATWDSKTETL--QNA 392
QY 181 RVSILPLERKDSYELQVAGPMPGSSYQGTWSEMSDPVIFOTQSEELKEGNPHLL 240
DB 393 HSMALPALLE--PSTRYMARVAV-RTSRGYNGIWMSEARSMDTES--VLPMTVALIV 447
QY 241 LLLLVIFIP-AFMSLKTPLMLRMKKIWAVPSEPRFFMPLYKCGSGDFKMW---VGAP 295
DB 448 IFLTIAVLALRFGLGYRLRRKWEKIPNPSKSHLFQ-----NGSAELMPGSMGAF 501
QY 296 FTGSSLBELGPMWS---PEV-----PSTLE--VYSGHPPSPAKRLQUTLEOE 336
DB 502 TSSGPPHQGPMGSRFPBELGVFPVGFDSSEVSPLTIEDPKHVCDDPPSGDPTTPAASDLPT 561
QY 337 PAELVESDGVKPSFPMPTAONSGSAYSEERDRPYGLVSDTVTLDAEGCTWP---CS 393
DB 562 EQPSPQGPAPPAHTEPKQASS-----FDNNGYLDGPPHRS 599
QY 394 CEDD-GYPALDLDAGLEBSP---GLEBDPLDAGTTVLSGCCVSAAGSPGLG-----G 440
DB 600 LPDILGQPEPPEQSGSKSPPGSLLEYLCLPAGGQVQLVPLAQMGQCAVEVERRPSQG 659
QY 441 PLGSLDLRLKRPPLADGEDMAGGLPMGGRSP-----GVSESEAGSLAGLMDPTPSG 493
DB 660 AAGS-----PSTLSG-----GGAPALGPVGGQDQKSPVAIPMSGGTDEDPG 704
QY 494 FVSGDCSSPVECDFT-----SPGDEGPPRSYLURQ 522
DB 705 -VASGYVSSADLVTPTPNSGASSVSLVPSLGLPSDQTPSLCPGLASGPPGAGPVKSGREG 763
QY 523 WVVIIP-----PLSSPGP 535
DB 764 YVELPPIEGRSRSPRNNPVP 784

RESULT 12
US-10-669-920-299
Sequence 299, Application US/10669920
Publication No. US20060194265A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Malandro, Marc S.
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
CURRENT APPLICATION NUMBER: US/10/669,920
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: US 10/004,113

PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 10/052,482
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 09/997,722
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 10/085,117
PRIOR FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 10/087,192
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: US 10/322,696
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 299
LENGTH: 895
TYPE: PRT
ORGANISM: Homo sapiens
US-10-669-920-299

Query Match 7.0%; Score 206; DB 6; Length 895;
Best Local Similarity 22.9%; Pred. No. 2.2e-08;
Matches 142; Conservative 66; Mismatches 225; Indels 188; Gaps 31;

QY 22 DLVCTDYLTQVTCILEMMNLHPSTLT-LTWODYBELKDEATSC-----SLHSAH- 72
DB 245 NLECFPGGAVALSCSWEKREKVASVSFGLFYKPSPDAGEBEGSPVLRGLSLHTRHHC 304
QY 73 -----NATATYTCCHMDVFHFMAADIFSVNITQSGNYSQECGSLIAESIKAPPPNV 126
DB 305 QIPVPDPATHGQY-----IVSV-----QPRRAEKHKS---SVNIQMAPP-SL 343
QY 127 TWTFSG-QYNISW-----RSDYEDPAFYMLKGKLOLEYQYNNRGDPMASPRKLIYSVS 180
DB 344 NVTKDGSYSILRWETMKRYEHIDHTF-----EIQYKDDATWDSKTETL--QNA 392
QY 181 RVSILPLERKDSYELQVAGPMPGSSYQGTWSEMSDPVIFOTQSEELKEGNPHLL 240
DB 393 HSMALPALLE--PSTRYMARVAV-RTSRGYNGIWMSEARSMDTES--VLPMTVALIV 447
QY 241 LLLLVIFIP-AFMSLKTPLMLRMKKIWAVPSEPRFFMPLYKCGSGDFKMW---VGAP 295
DB 448 IFLTIAVLALRFGLGYRLRRKWEKIPNPSKSHLFQ-----NGSAELMPGSMGAF 501
QY 296 FTGSSLBELGPMWS---PEV-----PSTLE--VYSGHPPSPAKRLQUTLEOE 336
DB 502 TSSGPPHQGPMGSRFPBELGVFPVGFDSSEVSPLTIEDPKHVCDDPPSGDPTTPAASDLPT 561
QY 337 PAELVESDGVKPSFPMPTAONSGSAYSEERDRPYGLVSDTVTLDAEGCTWP---CS 393
DB 562 EQPSPQGPAPPAHTEPKQASS-----FDNNGYLDGPPHRS 599
QY 394 CEDD-GYPALDLDAGLEBSP---GLEBDPLDAGTTVLSGCCVSAAGSPGLG-----G 440
DB 600 LPDILGQPEPPEQSGSKSPPGSLLEYLCLPAGGQVQLVPLAQMGQCAVEVERRPSQG 659
QY 441 PLGSLDLRLKRPPLADGEDMAGGLPMGGRSP-----GVSESEAGSLAGLMDPTPSG 493
DB 660 AAGS-----PSTLSG-----GGAPALGPVGGQDQKSPVAIPMSGGTDEDPG 704
QY 494 FVSGDCSSPVECDFT-----SPGDEGPPRSYLURQ 522
DB 705 -VASGYVSSADLVTPTPNSGASSVSLVPSLGLPSDQTPSLCPGLASGPPGAGPVKSGREG 763
QY 523 WVVIIP-----PLSSPGP 535
DB 764 YVELPPIEGRSRSPRNNPVP 784

RESULT 13

US-10-669-920-295
; Sequence 295, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669, 920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004, 113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052, 482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997, 722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034, 650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085, 117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087, 192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322, 281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322, 696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 901
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-295

Query Match 6.9%; Score 204.5; DB 6; Length 901;
Best Local Similarity 23.7%; Pred. No. 2.9e-08;
Matches 121; Conservative 51; Mismatches 186; Indels 153; Gaps 25;

QY 117 SIKAPPNNVTYTSQ-QYNISW-----RSYEDPAFMYLKGLOLYQYNNRDDPAVVS 170
DB 341 NIDAMP-SLNVTDGDSYSLRMETMKRYEIHDTF-----EIYKDOTATWDS 390
QY 171 PRRLISVDSRSVSLPLEPRKSSYELQVAPGMPGSSYOGTSEMSDPVITFOTSEEL 230
DB 391 KTEL--QNAHSMALPALE--PSTRYMARVAV-RTSRGYNGISENSEASMTDES--V 443
QY 231 KEGNPHLLLLLVIVFIP-AFWSLKTHTPLMLMKKIWAVSPDERFMPLYKGCSDGFX 289
DB 444 LPMWVLLVIFLFIIVALLALRFGIGYRLRRKWEKIPNPSKSHLFQ-----NSAB 497
QY 290 KW-----VGAPPTGSLGLPWS---PEV-----PSTLE--VTSCHPSPSPA 326
DB 498 LMPGSSAFTSGSPHQPWGSRRFPELEGVFPVGFGESEVSPITIEDPKVCDPSPGPD 557
QY 327 KRLQLTLEGEPAELVESDGVKPSFMPPTAONSGGSAVSEERDRPYGLVSDITVTLDAEG 386
DB 558 TTPAASDLPTBQPPSPQGPAPASHTEPKQAS-----PDPNG 595
QY 387 PCTWP---CSCCEDD-GYPALDLDAGLEBSP---GLEPDLDACTTVLSGCVSAGSPGLG 439
DB 596 PYLGPHSRSLPDLTIGPEPQEGSQKSPPGSLLEYLCLPAGGOVQLVLAQMGPQA 655
QY 440 -----GRLGLDLRLKPLPLADGEDMAGLEWGRSP-----GVSSEASGSPLA 483
DB 656 VEVERRDSQGAAGS-----PSLESG-----GGAPALAPRVGGODQKDSVPAIP 700
QY 484 GLMDTDFDSGFVSGDCSSPVECDFT-----SPGD 512
DB 701 MSSGDTDPG-VASGYSSADLVFTPNSGASSVLSGLPSDQTSCLGLASGPPGA 759
QY 513 EGPPRSYLRQWVVIIP-----PLSSPGP 535
DB 760 PGFVKSQFEGVELPPIEGRSRSPRPNVP 750

RESULT 14
US-10-505-928-650
; Sequence 650, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505, 928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363, 019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 650
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-650

Query Match 6.5%; Score 193.5; DB 6; Length 825;
Best Local Similarity 21.8%; Pred. No. 2e-07;
Matches 161; Conservative 69; Mismatches 220; Indels 289; Gaps 42;

QY 17 GMGCPDLV-----CYTDVLOTVICLEWMLHPST-----L 47
DB 2 GMLCSGLLPVUSCLVLLQASGSMKVLQEPCTVSDTMSISTC---EKKANGPTNCSTEL 58
QY 48 TLTWQDYEEELKDEATSCSLHRSANHTATYTCMDVHFHMAADIFSVNITDQSGNYSQ 107
DB 59 RLXYQLVF--LISBAHTC-----IPENNAGAGCVCHL-----LMDDVVASD-----NYTL 101
QY 108 EC-----GSFLAESIKPAPPPVTV--TFSGYINISMSDVEDPAFYMLKGLOLY 156
DB 102 DLWAGQQLMKSGSPSEHVKPPAPGNLTVHTVNSDITLITWNSPY--PDDNYLYNHLTY 159
QY 157 ELQYRRNGDPMWAVSPRKLISVDSRSVSLPLE-----PRKSSYELQVAPGMPG 207
DB 160 AVINWSNDP-----ADFRIVYTVLPSLRILASTLKGISTYARARAW--A 205
QY 208 SSYOGTSEMSDPVITFOTSEELKEGWNPHLLLVIVFIPAFWSLKTHTPLMLWKI 267
DB 206 QCVYTTSEMSPTKMH--NSYREPREQHLILGVSVSCVILAVCLCVSITIKIEXW 262
QY 268 W-AVSPDERFEM-----PLYKGC-----S 285
DB 263 WDQIPNPARSRILVAIIIQDAQSQWEEKRSRGDEPAKCPHMKNCITLKLPCFLEHMKRDE 322
QY 286 GDFRKXWGAPEFTGSSLEGPMSF-EV-----BSTLEVYSCHPRSPARKLQLTLEOE-P 337
DB 323 DPHAAKEMFPQSGG--KSAMCPEVEISKTVLMBESISVVR-----VELFEAP 368
QY 338 AELVESDGV--PKSPFWPTAONSGGSAVSEERDRPYGLVSDITVTLDAEG----- 386
DB 369 VECEEEVEVEEKSGFSPASSRSD--FOEGRE--GIVARLTRESLFLDLGGEENGFCQ 424
QY 387 -----PCTWPCSED-----DGYPALDLDAG-----LESPG----- 413
DB 425 QDMGESCLLPSPSGTSAHMPWDEFPS---AGKEAPAPWKEOPLHLEBPSPASPTQSPD 480
QY 414 -----LEPDLDACTTV--LSCGCVSAGSPGLGP---LGLSLDLRLKP----- 451
DB 481 NLCTETPLVIAQNPAYRSPSNLSOSPCCRELGPDLPLRLHLEVEPEMPCVPQUSEPT 540
QY 452 --PLADGEDV-----AGGLPWCGRSPG--GVSESEAG--SPLAGL----- 485
DB 541 TVQOPPEETWEOILRRNVLOHGAALAPVSAPTSGYQEFVAVAVOGGQVQASVGLGPGE 600
QY 486 -DMTDFDSGFVSGDCSSPVECDFTS-----PDGCPSPSYLRQWVVIIP 527
DB 601 AGYKAF--SSILASAVSPKCGFGASSGEGYKRPQDLIPGCGDPAF-----VP 649

QY 528 PLSPPG-----POAS 538
DB 650 VPLFTFGIDRPPRSPSS 668

RESULT 15

US-10-511-937-3001
; Sequence 3001, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Mohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3001
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-3001

Query Match 6.5%; Score 193.5; DB 6; Length 825;
Best Local Similarity 21.8%; Pred. No. 2e-07;
Matches 161; Conservative 69; Mismatches 220; Indels 289; Gaps 42;

QY 17 GWCGRDLV-----CTDYLQVLCILEMNLHPST-----L 47
DB 2 GMLCSGLLPVSCVLQVASSGNMKVLQEPCTVSDVMSISTC--EWMKMGPTNCSSTEL 58
QY 48 TLTWODQYEELKDEATSCSLHRSANATHATYTCMDVHFHMADDIFSVNITDQSNYSQ 107
DB 59 RLKYQLVY--LLSEAHTC---IPENNGACVCCHL-----LMDVVSAD-----NYTL 101
QY 108 EC-----GSFLAESIKPAPPFNTV--TFSGQYNISMRSDYEDPAFYMLKGLQY 156
DB 102 DLMAGQQLLMKGSFSPSEHVKPRAGNLTVHTNVSDTLLTWMSNPY--PPDNVLYNHLTY 159
QY 157 ELQYRNKGDPMWAVSPRKLIVSDRSVSLPLE-----FRKDSYELQYVAGPMPG 207
DB 160 AVNIMWSENDP-----ADPFIYNTVYLBPSLRIAASTLKSISYRARVRAM--A 205
QY 208 SSYOGTSEWSDPVYIFOTQSEELKEGNNPILLLLLVIFIPAFMSLKTBPMLRMKXI 267
DB 206 QCYVTTTSEWSPSTKM--NSYRPFQHLILGVSVCIVTILAVCLCYVSTIKIKEM 262
QY 268 W-AVSPSPERFPM-----PLYKGC-----S 285
DB 263 WDOIIPNPARSLVAILIIODAQSQWEKRSRGQEPKCPHMKNCLTKLPCFLEHMKRDE 322
QY 286 GDFKKTAVAPFTGSLLELGPWSP--EV-----PSTLEVYSCHPRSPAKRLQTLTELQ--P 337
DB 323 DPHKAAKEMPFQSG--KSAMCPVEISKTVLMPESISIVRC-----VELFEAP 368
QY 338 AELVESDGV--PKPSFMPTAONGSAYSEERDRPYGLVSDITVTV--LDAEG----- 386
DB 369 VECSEEEVEEBEKSGFSCASPESSRD--FOBGR-----GIVARLTESTFLDLGEEENGRCFQ 424

QY 387 -----PCTWPCSCED-----DGYPALDLADG-----LEPSDG----- 413
DB 425 QDMGESCLPPSGSTSAHMPWDERPS-----AGPKEAPWKGEOPLHLEPSFPASPTQSPD 480
QY 414 ----LEBDPLDAGTTV--LSCGCVSAGSPGLGSP--LGSLLRLKP----- 451
DB 481 NLCTETPLVIAGNPAVRSFNSLSQSPCPRLEGPDPILLARHLEVEBEMPCVPQLSEPT 540
QY 452 --PLADGEDW-----AGGLPWGGRSPG---GVSESEAG---SPLAGL----- 485
DB 541 TVQPPEPETWEQILRRNVLOHGAAPVSAPTSGYQEFVHAVEQGTQASAVVGLGPPGE 600
QY 486 -DMDTPDGFVSGDSCSPVECDFTS-----PGDEGPPRSYLRQWVYIP 527
DB 601 AGYRAF--SSLIASSAVSEBKCGFASSGEBSGYKFPQDLIPCGPDDPAB-----VP 649
QY 528 PLSPPG-----POAS 538
DB 650 VPLFTFGIDRPPRSPSS 668

Search completed: September 7, 2006, 12:58:47
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